

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 10:10:05 ; Search time 1326 Seconds

(without alignments)
167.217 Million cell updates/sec

Title: US-10-659-199-18

Perfect score: 2217

Sequence: 1 MAAAMAATTMTYTKNNRASLV.....TETGAGGQAAPKSGNDPR 433

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_03:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1906.5	86.0	396	2	Q6E5A5
2	1549	69.9	425	2	Q6Z782
3	1401.5	63.2	436	1	B7I_MALZE
4	1318.5	59.5	419	2	Q65XJ8
5	1192	53.8	415	2	Q65XJ8
6	1082.5	48.8	385	2	Q92NY4
7	1041	47.0	392	2	Q92NY4
8	580	26.2	238	2	Q8W008
9	563.5	25.4	385	2	Q6YZW6
10	561.5	25.3	346	2	Q8LJ38
11	561.5	25.3	348	2	Q9LJX5
12	464	20.9	318	2	Q8R0Y8
13	463	20.9	338	2	Q7RXJ3
14	462.5	20.9	352	2	Q04619
15	461	20.8	355	2	Q6T583
16	457	20.6	458	2	Q705K4
17	457	20.6	477	2	Q6NWK1
18	457	20.6	477	2	Q6NWK1
19	454	20.5	475	2	Q18757
20	452.5	20.4	515	2	Q69X19
21	450	20.3	318	2	Q86VD7
22	450	20.3	467	2	Q6GQ51
23	450	20.3	475	2	Q7TFC2
24	450	20.3	475	2	Q8BMD8
25	448	20.2	384	2	Q96N04
26	448	20.2	468	2	Q96N04
27	446.5	20.1	322	2	Q9T082
28	442	19.9	477	2	Q66L49
29	440.5	19.9	524	2	Q7PNW8
30	437	19.7	326	2	Q12251
31	436	19.7	476	2	Q6Z790

Result ID	Score	Query Match	Length	ID	Description
32	435	19.6	316	2	Q9N137
33	432	19.5	338	2	Q6C3A2
34	428.5	19.3	365	2	Q8W4M2
35	428.5	19.3	473	2	Q7R0U6
36	427.5	19.3	487	2	Q9T143
37	427.5	19.3	501	2	Q6NKM8
38	427.5	19.3	514	2	Q8JZT8
39	427.5	19.3	515	2	Q80T78
40	426.5	19.2	469	2	Q8K3P6
41	426	19.2	305	2	Q86DE1
42	425.5	19.2	337	2	Q8L7R0
43	425.5	19.2	367	2	Q6Z763
44	425.5	19.2	337	2	Q8VBT4
45	425.5	19.2	502	2	Q8BH0

ALIGNMENTS

RESULT 1

Q6E5A5 PRELIMINARY; PRT; 396 AA.

AC Q6E5A5; 25-OCT-2004 (TREMBLrel. 28, Created)

DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)

DE Plastidial ADP-glucose transporter.

OS Hordeum vulgare var. distichum (Two-rowed barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;

OC Triticeae; Hordeum.

NCBI_TaxID=112509;

RM [1]

RP SEQUENCE FROM N.A.

RX PubMed=1529120; DOI=10.1104/pp.104.045203;

RA Paton N.J., Greber B., Fahy B.F., Laurie D.A., Parker M.L., Denyer K.;

RT "The Iyves Mutations of Barley Reveal the Nature and Importance of Plastidial ADP-Glc Transporters for Starch Synthesis in Cereal Endosperm.";

RL Plant Physiol. 135:2088-2097(2004).

CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.

DR GO; GO:0005739; C:mitochondrion; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0005351; F:sugar porter activity; IEA.

DR GO; GO:0006839; F:mitochondrial transport; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR001893; MitoC_carrier.

DR InterPro; IPR002067; Mlt_carrier.

DR InterPro; IPR002030; Mlt_uncoupling.

DR Pfam; PF00153; Mito_carr; 3.

DR PRINTS; PRO00926; MITOCOUPLING.

DR PRINTS; PRO00784; MITOCOUPLING.

DR PROSITE; PS50920; SOLCAR; 3.

KW Sugar transport; Transmembrane; Transport.

SEQUENCE 396 AA; 42436 MW; 37EE334FDE24FB8D CRC64;

Query Match 86.0%; Score 1906.5; DB 2; Length 396;

Best Local Similarity 92.3%; Pred. No. 3.1e-136;

Matches 373; Conservative 7; Mismatches 15; Indels 9; Gaps 1;

QY 1 MAAAMAATTMTYTKNNRASLVMDKKMLRPVEVAFPMSSQPSRSLLDFPRALFASVGL 60

DB 1 MAAAMAATTMTYTKNNRASLVMDKKMLRPVEVAFPMSSQPSRSLLDFPRALFASVGL 60

QY 61 SLSHGAPVAREHDKAPADDDVAHQLLAAGEAGYQKAKKAKKQQLSLRKVRKIGN 120

DB 61 SLH-----HKGKAPADDDVAHQLLAAGDAGYQKAKKAKKQQLSLRKVRKIGN 111

QY 121 PHLRLVSGALAGAVSRFVAPLEFTRHLMVSGSGADSMGVFRIMRTGMPGLFIGN 180

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Db 112 PHLRRLVSGAIGAVSRTPVAPLETIRTHLMVSSGADSMGQVRRIMRTGEMGLFRGN 171
Qy 181 AAVNVLRAVPSKAIHFHYTDRAKKYLTPBAGPAPVPIPTPLVAGALGVASTLCTYEMEL 240
Db 172 AAVNVLRAVPSKAIHFHYTDRAKKYLTPBAGPAPVPIPTPLVAGALGVASTLCTYEMEL 231
Qy 241 VKRRLTEKVDYDNLHAFVKIVDRBEGPGLYRGLASLIGVVPYAAANFYAYETTLRGVY 300
Db 232 VKRRLTEKVDYDNLHAFVKIVDRBEGPGLYRGLASLIGVVPYAAANFYAYETTLRGVY 291
Qy 301 PRAASKEEVGNVPTLLIGSAGAIATATPPLVARRKQMGVAGRGQYKKNVLAHMYCI 360
Db 292 PRAASKEEVGNVPTLLIGSAGAIATATPPLVARRKQMGVAGRGQYKKNVLAHMYCI 351
Qy 361 LEKEGTAGLYRGAGPSCTIKLMPAAGISFMCYEACCKILVDEKED 404
Db 352 LNREGAAGLYRGAGPSCTIKLMPAAGISFMCYEACCKILINNOB 395

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RESULT 2

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ID Q62782 PRELIMINARY; PRT; 425 AA.
AC Q62782;
DT 05-JUL-2004 (TREMBlrel, 27, Created)
DT 05-JUL-2004 (TREMBlrel, 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel, 27, Last annotation update)
DE Putative Brittle-1 protein, chloroplast.
GN Name=P0419A09.38; Synonyms=O01135_F06.4;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP004065; BAD15497.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005743; C: mitochondrial inner membrane; IEA.
DR GO: GO:0005739; C: mitochondrial inner membrane; IEA.
DR GO: GO:0005488; F: binding; IEA.
DR GO: GO:0006839; P: mitochondrial transport; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; Mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS50920; SOLCAR; 3.
KW Transmembrane; Transport.
SQ
SEQUENCE 425 AA; 45363 MW; 2089820220BF2CA1 CRC64;

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Query Match 69.9%; Score 1549; DB 2; Length 425;

Best Local Similarity 75.2%; Pred. No. 4.5e-109; Indels 34; Gaps 8;

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Qy 1 MAAMAATTWTKNNR-----ASLVMDKKNNVLRVPEVAPFWS-----QPSRSIDFP 50
Db 1 MAAMAATTWTKNNR-----ASLVMDKKNNVLRVPEVAPFWS-----QPSRSIDFP 57
Qy 51 RRA---LFAVSGISLHGAAPVAREHDKARPADVVAHOLA--AGEAGVQRAQAK-K 103
Db 58 RRAAPPLFAVSGISLHGAAPVAREHDKARPADVVAHOLA--AGEAGVQRAQAK-K 108

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Qy 104 AKKOQLSRKRVKIGNPHLRRLVSGAIGAVSRTPVAPLETIRTHLMVSSGADSMAGV 163
Db 109 GGGGLSLRKVRVKIGNPHLRRLVSGAIGAVSRTPVAPLETIRTHLMVSSGADSMAGV 168
Qy 164 FRIMRTGEGWPGFLFRGNAAVNLRAVPSKAIHFHTYTDRAKKYLTPBAGPAPVPIPTPLVA 223
Db 169 FRIMRTGEGWPGFLFRGNAAVNLRAVPSKAIHFHTYTDRAKKYLTPBAGPAPVPIPTPLVA 228
Qy 224 GALAGVASTLCTYEMELVTRLTIEKVDYDNLHAFVKIVDRBEGPGLYRGLASLIGV 283
Db 229 GALAGVASTLCTYEMELVTRLTIEKVDYDNLHAFVKIVDRBEGPGLYRGLASLIGV 288
Qy 284 PYAANFYAYETTLRGVRRASGKEEVGNVPTLLIGSAGAIATATPPLVARRKQMGV 343
Db 289 PYAATFYAYETTLRLRYRATGRADVGPATLLIGSAGAIATATPPLVARRKQMGV 348
Qy 344 VGGROYKKNVLAHMYCILEKEGTAGLYRGAGPSCTIKLMPAAGISFMCYEACCKILVDEKE 403
Db 349 VGGROYKKNVLAHMYCILEKEGTAGLYRGAGPSCTIKLMPAAGISFMCYEACCKILVDEEB- 407
Qy 404 DGAAREPQETENGQ 418
Db 408 ---AAPELEAECAE 418

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RESULT 3

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ID BT1_MAIZE STANDARD; PRT; 436 AA.
AC P29518;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Brittle-1 protein, chloroplast precursor.
GN Name=BT1;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACOCD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93005685; PubMed=1668652;
RA Sullivan T.D., Strelow L.I., Illingworth C.A., Phillips R.L.,
RA Nelson O.E., Jr.;
RT "Analysis of maize brittle-1 alleles and a defective suppressor-
RT mutator-induced mutable allele.";
RL Plant Cell 3:137-1348(1991).
CC -1- FUNCTION: Could play a role in amyloplast membrane transport.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast inner
CC membrane; amyloplast inner membrane (Potential).
CC -1- TISSUE SPECIFICITY: Endosperm of developing kernels.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -1- SIMILARITY: Contains 3 Solcar repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL: M79333; AAA33438.1; -.
DR EPR; J01459; J01459.
DR MaizeDB; 47578; -.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; Mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS50920; SOLCAR; 3.
KW Amyloplast; Chloroplast; Inner membrane; Repeat; Transit peptide;
KW Transmembrane; Transport.
FT TRANSIT 1 75 Chloroplast (Potential).

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FT	CHAIN	76	436	Brittle-1 protein.
FT	TRANSMEM	229	247	Potential.
FT	TRANSMEM	327	347	Potential.
FT	REPEAT	132	216	Solcgr 1.
FT	REPEAT	227	311	Solcgr 2.
FT	REPEAT	324	412	Solcgr 3.
SO	SEQUENCE	436 AA;	46627 MW;	9600C05F603BD4E CR664;

Query Match	63.2%;	Score 1401.5;	DB 1;	Length 436;
Best Local Similarity	65.4%;	Pred. No. 7.1e-98;		
Matches 291;	Conservative 46;	Mismatches 69;	Indels 39;	Gaps 9

Qy	1	MAAAMAAATVTKNNRAALVMDKKMILLRPEVEVAFPMSSQ--PEKSLDFPPRALFASVG	59
Db	1	MAATMAATVTVNTR-----KESMSLQVAVAFPMKPRGGKTGGLEPPRRAMFASVG	52
Qy	60	LSLSHGAP--VAREHDG-ARPAD--DYAHOLAAAGEAGVOKAKAKAKKQOJSLKRV	114
Db	53	LNVCPGVAGRDPREPDPKVVPAALNCIPLAALPPFAPSRRPPCGRGSRGSEEEAGRGSH	112
Qy	115	RVKIG-----NPLRLVSGAIGAVSRTPVAPLETRTHLMGSSGADSM	160
Db	113	EEAAAAGSEEBEGGQDORQAPAPALVSGALIGAVSRTPVAPLETRTHLMGSSICVDNM	172
Qy	161	AGVFRMIRTEGMPGLFRGNANVNLVVAAPSKAIIEHTYDTAKKYLTPAEGEAPAKVPIPTP	220
Db	173	AGVFQWIMQNGMTSLFRGNANVNLVVAAPSKAIEHTYDTAKKFLTPKGDPEPKPIPTP	232
Qy	221	LVAGALAGVAATLCITYPMELVYTRLTLEEDVDYDNLHAHVKIVRDEGPEELYRGLAPSLI	280
Db	233	LVAAGLAFPAATLCITYPMELIKTRYLTLEEDVDYDNLHAHVKILRDEGPEELYRGLTPSLI	292
Qy	281	GVPVPAALNFAVETLRGVYRRARASGE---EYGNVPTLLIGSAGAIASTATPPELVARK	337
Db	293	GVPVPAALNFAVETLRKLYRATGRRRPPADVGPATLLIGSAGAIALASATPPELVARK	352
Qy	338	QMVGAVGGRQVYKNVLHAMYCILEKEGTAGLYRGISPCIKLMPAAGISFMCYEACCKI	397
Db	353	QMVGAVGGRQVYQNVLHAIYCIILKEKGAGGLYRGISPCIKLMPAAGIAFMCYEACCKI	412
Qy	398	LVDEKEDGGALEPQETETGQAQGG	422
Db	413	LVDEKED-----EEDEAG--GGE	429

RESULT 4			
ID	Q69XJ8	PRELIMINARY;	PRT; 419 AA.
AC	Q69XJ8;		
DT	25-OCT-2004 (TREMBLrel. 28, Created)		
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)		
DE	Putative mitochondrial energy transfer protein.		
GN	Name=P0486H12.22;		
OS	Oryza sativa (Japonica cultivar-group).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehartoideae; Oryzeae; Oryza.		
OX	NCBI_TaxID=39947;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Saeki T., Matsumoto T., Yamamoto K.;		
RT	"Oryza sativa nupribare (GA3) genomic DNA, chromosome 6, PAC		
RT	clone.P0486H12.";		
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: Belongs to the mitochondrial carrier family.		
DR	EMBL, AP003615; BAD53459.1;		
DR	GO: 0016020; C:membrane; IEA.		
DR	GO: 0005743; C:mitochondrial inner membrane; IEA.		
DR	GO: 0005739; C:mitochondrion; IEA.		
DR	GO: 0005488; F:binding; IEA.		
DR	GO: 0006839; P:mitochondrial transport; IEA.		
DR	GO: 0006810; P:transport; IEA.		

DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002067; Mlt carrier.
DR InterPro; IPR002030; Mlt_uncoupling.
DR Pfam; PF00153; Mltc_carrt_3.
DR PRINTS; PR00926; MITOCHARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PSS0920; SOLCAR; 3.
KW Transmembrane; transprot;
SEQUENCE 419 AA; 4538 MW; A4A9E8CAD32BAA CRC64;

Query Match	59.5%;	Score 1318.5;	DB 2;	Length 419;
Best Local Similarity	-64.6%;	Pred. No. 1.3e-91;		
Matches 270;	Conservative 47;	Mismatches 74;	Indels 27;	Gaps 7;

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Oy 10 MVTGNANSLAYMDCK-WMLRLPVEVAFPMSSQCE---SRSLD--EPRRLAFVGSLSL 62
Db 4 MSAKSKSVLTLEKKQGSVPQLELAFPMDLHEDKGSLSLHGSASBPHGLFASVGLVK 63
Oy 63 SHGAPVYA---REHDGKARPADDVAHQLA--GEAGVQKQAKAKK 106
Db 64 STAPAVAPSPAEDHFKLPADHCGIKVYSSAVGYQVPGTEASVNEEBEVDGKAVKAKK 123
Oy 107 QQSLRKRVKYLGNPHRLRLVSGAIAGVNSTPAPELITRTHLMGSSGADSMAGVPRW 166
Db 124 RGL---KLKIKIGNPHRLRLVSGVAAGVASTCAPELITRTHLMVGSNG--DSMTVEFQS 179
Oy 167 IMRTGEGPGIFRGNAVNVLRVAPSKALEHFYDPAKKYLFPPEAGEPAKVPPIPTLVAGAL 226
Db 180 IMKEGMTGIFRGNFVNVIRVAPSKALELFPDPAKKFLPTPKADESRKTPPPPSLIACAL 239
Oy 227 AGVASTLCYPMELVKTRLTTEKVDYDNLHAIFYKIVRDEGPGELYGLABSLIGVVPYA 286
Db 240 AGVASTLCYPMELIKTRLTEKVDYNNPPLHAIFYKILREBGPSELVYGLTSLIGVVPYA 299
Oy 287 AAFNYAYETLRGVTYRRASGKEEVGNVPTLLIGSAAGAIASATPTPLEYARQOMGVAGVG 346
Db 300 ATNYAYADTLKKLRYKFTKQEBELISNIATLLIGSAAGAISSATPTPLEYARQOMGVAGVG 359
Oy 347 RQYKKNVLLHMYCYLLEKEGTAGLYRGAGSPCKLMPAAGISFMYCYBAKCKLLVYDEKED 404
Db 360 RQYKKNVFNHAYCYIMENBEGIGGLYKGGASPCCKLMPAAGISFMYCYBAKCKLLVYEDDQ 417

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5	RESULT		
655XR7	065XR7	PRELIMINARY;	PRT; 415 AA.
AC	065XR7;		
DT	25-OCT-2004 (TREMBLrel. 28, Created)		
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)		
DE	Puative adenylate translocator (Brittle-1) protein.		
GN	Name=P0685E10.12;		
OS	Oryza sativa (Japontica cultivar-group) .		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae		
OC	Erihartoideae; Oryzeae; Oryza.		
OX	NCBI_TextID=39947;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Chow T.-Y., Hsiang Y.-I.C., Chen C.-S., Chen H.-H., Liu S		
RA	Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.		
RA	Chen Y.-L., Cheng C.-H., Chung C.-T., Han S.-Y., Hsiao S		
RA	Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-		
RA	Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S		
RA	Wu H.-P., Shaw J.-F.		
RT	"Oryza sativa PAC P0685E10 genomic sequence."		
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBD databases		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Chow T.-Y.;		
RL	Submitted (May-2004) to the EMBL/GenBank/DBD databases		
DR	EMBL; AC087553; AAU44334.1, -.		
SO	SEQUENCE 415 AA; 44028 MW; 3B7A32081CBF1B6 CRC64;		

Query Match 53.8%; Score 1192; DB 2; Length 415;
 Best Local Similarity 65.3%; Pred. No. 5.2e-82;
 Matches 235; Conservative 47; Mismatches 72; Indels 6; Gaps 2;

50 PRRLFFSVGL-----SLSHGAPVAREHDKAR-PADVAHQLAALAAEAGYQKAKKA 104
 57 PASGLFASVGVGPATSSSPSPDAPDPAKYAVSDEIEHMLPGOSVEVLEMEKCKN 116
 105 KKQOLSTRKVRKVGKGNHLRLVSGAIAAGVSRTEVPLETTIRTHLVWSSGADSMGVF 164
 117 KKKTNKFKKIKIKGNPHLKKLISGJAGAVSRATAVPLETIRKTHLVWSSG-NSTLEVF 175
 165 RWIRTEGMPGLFRGNAVNLVAVPSKAIEHFTYDTAKKYLTPRAGEPAKVP1PTPLVAG 224
 176 QSIKHKGWMTGLFRGNFVNVIKAVSKAIELFADDTANKFLTPRSGQKVPPLPSLVAG 235
 225 ALAGVASTLCTYPPELVYKTRLTITKDYNDILHAFVKIIVDEGEGELYRGLAPSLGV 284
 236 AFAGVSTLCTYPLELTKITRLTIORGVDNPLHVLVIEEGPTELRYGLTSLIGVP 295
 285 YAAAFAYETLRGVARRASGKEEVNPTLLIGSAGATASTATPPLVARKOMGVAV 344
 296 YAAITNPAVDLTKKAYKMKFTNIGVPTLLIGSAGATASTATPPLVARKOMGVAV 355
 345 GGRQVYKVLHAMYCIIEKGTAGLYRGLGPSCTIKLMPAAGISPMCEACKKILVDEKED 404
 356 GGRVYKVMHALLSLIEDSGVGLYRGLGPSCKMLVPAAGISPMCEACKKILTEBEDD 415

DB

345 GGRQVYKVLHAMYCIIEKGTAGLYRGLGPSCTIKLMPAAGISPMCEACKKILVDEKED 404
 356 GGRVYKVMHALLSLIEDSGVGLYRGLGPSCKMLVPAAGISPMCEACKKILTEBEDD 415

RESULT 6
 Q9ZNY4 PRELIMINARY; PRT; 385 AA.

ID Q9ZNY4
 AC Q9ZNY4
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)
 DE Mitochondrial energy transfer protein precursor.
 GN Name=Brict1el;
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN
 RP SEQUENCE FROM N.A.
 RA Rink U.A., Riesmeier J.W., Willmitzer L.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rink U.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the EMBL/GenBank/DBJ databases.
 DR EMBL; X98474; CAA67107.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mlt_carrier.
 DR Pfam; PF00153; Mito_car1; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PSS0920; SOLCAR; 3.
 KW signal; Transmembrane; Transport.
 FT SIGNAL 1 44 Potential.
 FT CHAIN 45 385 Potential.
 SQ SEQUENCE 385 AA; 41232 MW; 88716118792C0B84 CRC64;

Query Match 48.8%; Score 1082.5; DB 2; Length 385;
 Best Local Similarity 58.7%; Pred. No. 9.6e-74;
 Matches 222; Conservative 56; Mismatches 85; Indels 13; Gaps 5;

38 WSSQPESSRSLDFRRALFASV-----GLSLSHGAPVAREHDKAR-PADVAHQLAALAA 90

DB

9 WGSNGVSKIQTFVLVDLFAVGVGMGCVSSPNSSDSRDENGFKLPYSIDCKMYLSF 68
 91 GE----AGYQAKQAKKAKQOOLSTRKVRKVGKGNPHLRLVSGAIAAGVSRTEVPADLETT 146
 69 SEGFKIVNGEERGCVYKCKKKKGL-KIKLVSNPDLRLRLISALIGALSRTVAALGLTI 127
 147 RTHLVWSSGADSMAGVFPFIMRTGMPGLFRGNAVNLVAVPSKAIEHFTYDTAKKYL 206
 128 RTHLVWSSG-HSSTEVFNISIMTEGWTGLFRGNFVNVIKAVSKAIELFVYDTVANKNIS 186
 207 PEKGPAKVP1PTPLVAGALAGVASTLCTYPPELVYKTRLTITKDYNDILHAFVKIIVRDE 266
 187 SKPGEOSKIP1PISLVAGACAGVSTLLYPLELVTTRLTIORGVDNGLDAFVKLKEG 246
 267 GPGLRGLAPSLIGVFPYAAAFYAYETLRGVARRASGKEEVNPTLLIGSAGATAS 326
 247 GPALRYGLTSPYISGIPYAAATYFPAYDSLRKRYKIFKEBKIGNLETLLIGSAGATAS 306
 327 TATPPLVARKOMGVAGRGYKVLHAMYCIIEKGTAGLYRGLGPSCTIKLMPAAGI 386
 307 TATPPLVARKOMGVAGRGVAVKIVHVALVSLIEQDIGHLYKGLGPSCKMLVPAAGI 366
 387 SPMCEACKKILVDEKED 404
 367 SPMCEACKKILTEBEDD 415

DB

387 SPMCEACKKILVDEKED 404
 367 SPMCEACKKILTEBEDD 415

RESULT 7
 Q9SU1 PRELIMINARY; PRT; 392 AA.

ID Q9SU1
 AC Q9SU1
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Adueny1ace translocator (Btittle-1)-like protein
 DE (AT9432400/F8B4_100).
 GN Name=F8B4_100; Synonyms=AT9432400;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN
 RP SEQUENCE FROM N.A.
 RA Bevan M., Terry N., Ardiles W., Buysbaert C., Daseville R.,
 RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
 RA Villarejo R., Gielens J., Van Montagu M., Hohensei J., Mewes H.W.,
 RA Mayer K.F.X., Lemcke K., Schueller C.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Terry N., Ardiles W., Buysbaert C., Daseville R., De Clerck R.,
 RA De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarejo R.,
 RA Gielens J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
 RA Carinci P., Chang B., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.U., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:22088475; PubMed:12093376;
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldman K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 annotation.";
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Shlun P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
 RA Bowser L., Carlini P., Chung M.K., Goldsmith A.D., Hayaishiaki Y.,
 RA Ishida J., Jones T., Kamuya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinzaki K.,
 RA Davis R.W., Theologis A., Becker J.R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 DR EMBL, AL034567; CAA23567.1; -;
 DR EMBL, AL161581; CAB79957.1; -;
 DR EMBL, AY074831; AAL69529.1; -;
 DR EMBL, AY084938; AAM61499.1; -;
 DR EMBL, AF372944; AAK50084.1; -;
 DR PIR, T05350; T05350.
 DR GO, GO:0016021; C:integral to membrane; IEA.
 DR GO, GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO, GO:0005488; F:binding; IEA.
 DR GO, GO:0006810; F:transport; IEA.
 DR InterPro, IPR001993; Mitoch carrier.
 DR InterPro, IPR002067; Mitoch carrier.
 DR Pfam, PF00153; Mito carri; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE, PS50920; SOLCAR; 3.
 KW Transmembrane; Transport.
 KW SEQUENCE 392 AA; 42571 MW; 556269D8C67640C2 CRC64;
 SQ
 Query Match 47.0%; Score 1041; DB 2; Length 392;
 Best Local Similarity 64.9%; Pred. No. 14e-70;
 Matches 203; Conservative 47; Mismatches 59; Indels 4; Gaps 2;

Q8W008
 ID Q8W008 PRELIMINARY; PRT; 238 AA.
 AC Q8W008;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Britle-1-like protein.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 ON NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=seed endosperm;
 RA Villand P., Kleczkowski L.A.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AY031629; AAK55487.1; -;
 SQ SEQUENCE 238 AA; 25508 MW; 6CAD5AF88236E43D CRC64;
 Query Match 26.2%; Score 580; DB 2; Length 238;
 Best Local Similarity 55.9%; Pred. No. 6.8e-36;
 Matches 138; Conservative 14; Mismatches 67; Indels 28; Gaps 5;

QY 1 MAAATAATMTYKNNRASILVMDKKWLRPVPEVAFPPSSQPSRSLDPPRALFASVGL 60
 DB 1 MAAATAATMTYKNNRASILVMDKKWLRPVPEVAFPPSSQPSRSLDPPRALFASVGL 60
 QY 61 SLSHGAPVAREHDKARPADVAHQLAAGAGVQKQAKKAKKQOLSLRKVRKIGN 120
 DB 61 SLSS-----HNGKARPADVFSHQLAAGAGVHQKQAKKAKKHLGLRKVRKIGN 111
 QY 121 PHLRLVSGAIAAGNSRFRVAPLETIRTHLMVGSSGADSMAGVFWIMRTGMP----- 174
 DB 112 PHLRLVSGAIAAGNSKQFRG-----AAGDQDPDGGKLRPLRGRGFPVDHAG 162
 QY 175 GLFRGNAVNVIRVAPSKAIE-HFTYDTAKKYLTTPAG--BPAPYIPPLVAGALAGA 230
 DB 163 GVARPLPRQKQRLPRXAEQGHRTIHLHGQEVPPDGGRRSQKYPPIPLRVAGALAGA 222
 QY 231 STLCTYP 237
 DB 223 QPCAPIP 229

RESULT 9
 Q6YZW6 PRELIMINARY; PRT; 385 AA.
 ID Q6YZW6;
 AC Q6YZW6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Putative mitochondrial energy transfer protein.
 GN Name=OJ1003 A09.8; Synonyms=P0689E12.32;
 OS Oryza sativa (Japanese cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzae; Oryza.
 ON NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saeki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nippondate (Ga3) genomic DNA, chromosome 8, BAC
 RT clone:OJ1003 A09.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Saeki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nippondate (Ga3) genomic DNA, chromosome 8, PAC
 RT clone:P0689E12.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 DR EMBL, AP005509; BAD10433.1; -;

DR EMBL; AY085067; AAM61623.1; -.

CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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DR EMBL, AF000383; BAB01883.1; -.
DR EMBL, BT005998; AAO64933.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mito carrier.
DR InterPro; IPR002067; Mito carrier.
DR Pfam; PF00153; Mito car1.3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS50920; SOLCAR; 3.
DR Transmembrane; Transport.
SQ
SEQUENCE 348 AA; 37903 MW; D74019D16A5406 CRC64;

Query Match
Best Local Similarity 39.9%; Pred. No. 2.8e-34; Length 348;
Matches 117; Conservative 75; Mismatches 82; Indels 19; Gaps 5;

QY 124 RRLVSGAIGAVSRFPVAPLETIRTLMTVSSGADSMAGVFRWIMRTGMPGLFRGNAYN 183
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 50 REFLSGALAGMTKAVLALETIRTMIVG-VGSRRIPIPSFLEVQKQMGILMGNENIN 108
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 VLRVAPSKAIEHFTYDTAKKYLTP-----BAGEPAKVPFP-----TFL-VAGAL 226
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 109 MTRIIPTQAIIEGTFFEWVKRAMTSAQVKLKIEDAKIEIGDSFSPSISWISFVAVAGAS 168
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 227 AGVASTLCYPMELVTKRLTIEDVYDNLHAFAVKIVRDEGPELVRGLAPSLIGVVPYA 286
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 169 AGIASTLVCHPLEVLKDLRLVSPSEIPLSLAIPLFRADGIRGFAGLPTLVGMLPYS 228
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 287 AANFAYETLRGVYRRASKEEVGNPTLLIGSAGAIATATPFLPLEVARKOMOVAGVG 346
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 229 TCYYFMYDMKSYCKSKKKAALSREMLVLGALAGLTASTISFLEVARKKLMVAGALNG 288
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 347 ROYKYNVLHAMYCIIEKEGTAGLYRGLGPSICIKLMPAGISFMCYEAACKIIV 399
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 289 -ECPNMAAIAEVVYKGGVGLYRGWGASCIKVPSSGITWVFYEWKDIIL 340
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
Q8R0Y8 PRELIMINARY; PRT; 318 AA.
AC Q8R0Y8;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feltingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Ronaldo M.F., Cavaant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Murzy D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.;
"Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Struhsberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
DR EMBL; BC025937; AAH25937.1; -.
DR HSSP; P02722; 10KC.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002099; DNA mis repair.
DR InterPro; IPR002167; Graves DC.
DR InterPro; IPR001993; Mito carrier.
DR InterPro; IPR002067; Mito carrier.
DR Pfam; PF00153; Mito car1.3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00058; DNA MISMATCH_REPAIR_1; UNKNOWN_1.
DR PROSITE; PS50920; SOLCAR; 3.
DR Hypothetical protein; Transport.
SQ
SEQUENCE 318 AA; 35241 MW; 28350DD1C41199BD CRC64;

Query Match
Best Local Similarity 34.1%; Pred. No. 6.2e-27; Length 318;
Matches 113; Conservative 71; Mismatches 117; Indels 30; Gaps 8;

QY 74 DQKAPADVDVAHQLAAGAGVQKAKKAKQOLSRKVAKIGNPHLRVSGAIG 133
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 7 EGAVTLRED-----AEAVLAGVSSKRDHRYLS-----SLSGALNG 44
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 134 AVSRFPVAPLETIRTLMTVSSGADSMAGVFRWIMRT--EGMPGLFRGNAYNVLRVAPS 190
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 45 ALAKTAVAPLDRKTIIFQV-SKRSFAKAFLLVFTYINIEGFLSLMRGNSATWVRVIVY 103
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 191 KAIEHFTYDTAKKYLTPBAGEPAKVPITP-LVAGALGVASTLCYPMELVYKTRLT-I-E 248
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 104 AAIQPSAHEVEYKRIIGHYVFRGELPMPFRLLAGLAGLTGTAASLTYPDLVRARNAVTP 163
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 KDYVNDNLHAFKIVRDEGPELVRGLAPSLIGVVPYAANFAYETLRGVYRRASKEE 308
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 164 KEMSNIRHVFIRIRREBLKTLTFGFTVGLVPIYGLSFYTESLSLRREYSGRQ 223
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 309 VGNVPTLLIGSAGAIATATPFLPLEVARKOMOVAGVGRQYKYNVLHAMYCIIEKEGTA- 367
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 224 PVPFERMTVFGACAGIIGSASVPLDVRVRMGTAGVTGHQ-HGSTLSTLRSLVREBGNVR 282
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 368 GLYRGLGPSICIKLMPAGISFMCYEAACKIIL 398
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 283 GLYKGLSMNMWLKGPVAVGISFTTFLMQILL 313
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
Q7RXJ3 PRELIMINARY; PRT; 338 AA.
AC Q7RXJ3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feltingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Ronaldo M.F., Cavaant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Murzy D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.;
"Generation and initial analysis of more than 15,000 full-length human

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RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Iankiev P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Seltremkoff C.P., Kinner G., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kamal M., Kamysellis M., Mauceli E., Bielke C., Rudd S., Fishman D.,
 RA Krysstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmant S.A.,
 RA DeSouza C.C., Glass L., Obach M.J., Berglund J., Voelker R.,
 RA Yarden O., Flanagan M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Nativg D.O., Alex L.A., Mannheim G., Ebbels D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nisbaum C., Birren B.,
 RT "The Genome Sequence of the Filamentous Fungus *Neurospora crassa*."
 RL Nature 0:0-0(2003).
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABX0100743; EAA27338.1; -.
 DR HSSP; P02722; 10KC.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR002113; Aden translocator.
 DR InterPro; IPR001993; Mitoch carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; Mito_carr; 3.
 DR PRINTS; PR00927; ADPTRNSLCASE.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS50920; SOLCAR; 3.
 KM Hypothetical protein; Transmembrane; Transport.
 SQ SEQUENCE 338 AA, 36981 MW, 23982DA98ED2BA82 CRC64;

Query Match 20.9%; Score 463; DB 2; Length 338;
 Best Local Similarity 33.9%; Pred. No. 7.9e-27;
 Matches 104; Conservative 59; Mismatches 124; Indels 20; Gaps 7;

QY 115 RVIKGNPHRLRLVSGAAGAVSTFVAPLETRHLMVGGSGAD----SNAGVPRWIMRT 170
 DB 29 RSNVSOPTVAFAFCAGGAGVAVSRVVSPLRLKTLVQVSSGRAYKLVSQKALAKWRE 88
 QY 171 EGMFGPLRGNAVNVLRVAPSKALIEHPYDTAKKTLTPEAGEPKAVPIPTPLVAGALAGVA 230
 DB 89 EGMFGPAAAGNGTNCIRIVPISAVDFGSGYNPKRNIFRRHGDSTLP--SLTTCGLAGIT 147
 QY 231 STLCYPMELVKTRLTLEKVDYDNL-----LHAFYKIVRDEG--PGEELYRGLAPS 278
 DB 148 SVFTFYDLDIRTRLSIQTASFALGERPRMPGMEFTLVVMRTGEGFPA--LYRGIVPT 206
 QY 279 LIGVVPFAANFPAVETLRGVRRASKEVEGNVPTLLISAGALASTATPFLVARKQ 338
 DB 207 VAGVAPVGNLFWYEHVR--QYTLTDEQNPASVRKLIAGVAVQCTTYPEDVLR 265
 QY 339 MGVGAVGR--QVKNVLAHWYCTLEKEGTAGLVGLGSPGCKLMPAAGISFMCEACKKI 397
 DB 266 FQINTSGMGVQYKIGTDAVAVITEGIRGLYGIYFNLKVAIPMASSWISLEYCRDP 325
 QY 398 LVDEKED 404
 DB 326 LVGKPE 332

GN Name=A_IG002N01.16; Synonyms=AT4g01100, At4g01100;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 RX NCBI TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Scheet P., Magli L.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wash U;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J.M.,
 RA Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
 RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shin P.,
 RA Subhwick A., Davis R.W., Ecker J.R., Theologis A.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida U., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai U., Kim C., Lam B., Lin U.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shim P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida U., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai U., Lam B., Lee J.M., Lin U., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Lamar B., Stonelking T., Stumpf J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA ED Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 DR EMBL; AL161491; CAB80919.1; -.
 DR EMBL; AF412085; AAL06538.1; -.
 DR PIR; T01729; T01729.
 DR HSSP; P02722; 10KC.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR002113; Aden translocator.
 DR InterPro; IPR001993; Mitoch carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; Mito_carr; 3.
 DR PRINTS; PR00927; ADPTRNSLCASE.

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: May 25, 2005, 13:40:20 ; Search time 919 Seconds
(without alignments)
157.608 Million cell updates/sec

Title: US-10-659-199-18

Perfect score: 2217
Sequence: 1 MAAAMAATTMTVKNRSLV.....TENGAGQAPAKSSNGDRP 433

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published Applications AA.*

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16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US6_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2217	100.0	433	9	US-09-796-766-18
2	2217	100.0	433	15	US-10-659-199-18
3	1529	69.0	440	15	US-10-425-114-53253
4	1521.5	68.6	439	15	US-10-425-114-50902
5	1521.5	68.6	439	15	US-10-425-114-65995
6	1470.5	66.3	414	16	US-10-437-963-150460
7	1401.5	63.2	436	9	US-09-796-766-21
8	1401.5	63.2	436	15	US-10-659-199-21
9	1329.5	60.0	423	16	US-10-437-963-146611
10	1310	59.1	444	15	US-10-425-114-63026
11	1310	59.1	444	15	US-10-425-114-63935
12	1309	59.0	444	15	US-10-425-114-52078
13	1192	53.8	415	16	US-10-437-963-122416

14	1151.5	51.9	431	15	US-10-425-114-67044	Sequence 67044, A
15	1139.5	51.4	289	9	US-09-796-766-20	Sequence 20, Appl
16	1139.5	51.4	289	15	US-10-659-199-20	Sequence 20, Appl
17	1077	48.6	391	15	US-10-424-559-285116	Sequence 285116, A
18	1001	45.2	272	9	US-09-796-766-14	Sequence 14, Appl
19	1001	45.2	272	15	US-10-659-199-14	Sequence 14, Appl
20	792	35.7	273	15	US-10-424-559-265334	Sequence 265334, A
21	754.5	34.0	233	16	US-10-437-963-150461	Sequence 150461, A
22	740.5	33.4	231	16	US-10-437-963-150463	Sequence 150463, A
23	691	31.2	177	16	US-10-767-701-47449	Sequence 47449, A
24	595.5	26.9	337	16	US-10-437-963-118448	Sequence 118448, A
25	589.5	26.6	410	9	US-09-796-766-10	Sequence 10, Appl
26	589.5	26.6	410	15	US-10-659-199-10	Sequence 10, Appl
27	580.5	26.2	397	15	US-10-425-114-64610	Sequence 64610, A
28	574	25.7	375	16	US-10-767-701-43678	Sequence 43678, A
29	569	25.7	382	16	US-10-767-701-42759	Sequence 42759, A
30	565.5	25.5	378	15	US-10-424-559-240836	Sequence 240836, A
31	563.5	25.4	385	16	US-10-437-963-122906	Sequence 122906, A
32	502.5	22.7	267	15	US-10-424-559-241909	Sequence 241909, A
33	481	21.7	111	16	US-10-767-701-38030	Sequence 38030, A
34	474	21.4	345	15	US-10-424-559-221235	Sequence 221235, A
35	467.5	21.1	352	15	US-10-424-559-221242	Sequence 221242, A
36	466.5	21.0	391	15	US-10-425-114-55333	Sequence 55333, A
37	463	20.9	252	9	US-09-796-766-4	Sequence 4, Appl1
38	463	20.9	252	15	US-10-659-199-4	Sequence 4, Appl1
39	461	20.8	355	16	US-10-437-963-184488	Sequence 184488, A
40	459	20.7	109	9	US-09-796-766-16	Sequence 16, Appl1
41	459	20.7	109	15	US-10-659-199-16	Sequence 16, Appl1
42	458.5	20.7	413	15	US-10-425-114-55333	Sequence 55333, A
43	458.5	20.7	473	15	US-10-424-559-245081	Sequence 245081, A
44	457	20.6	477	9	US-09-777-921A-2	Sequence 2, Appl1
45	457	20.6	477	15	US-10-698-489-2	Sequence 2, Appl1

ALIGNMENTS

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RESULT 1
US-09-796-766-18
; Sequence 18, Application US/09796766
; Patent No. US20010047523A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Ralski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BBI157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Trillium aestivum
US-09-796-766-18

Query Match 100.0%; Score 2217; DB 9; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.7e-193;
Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMAATTMTVKNRSLVMDKQWLLRPVEVAFPMSSQPSRSRLDPPRRALFASVGL 60
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DB 1 MAAAMAATTMTVKNRSLVMDKQWLLRPVEVAFPMSSQPSRSRLDPPRRALFASVGL 60
  |||
QY 61 SLSHGAPVAREHDGKARPADVAHQAAGAGVQAKAKKAKQOQLKRVKYN 120
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Db 61 SLSHGAPPVAREHDKARPADDVAHQLAAGAGVQAKAKKAKKQOOLSIRKVRXIGN 120
Qy 121 PHLRIVSGAIIAGVSRTPVAPLETTIRTHLMVSSGSDSMAGVPRIMRTGMPGLFRGN 180
Db 121 PHLRIVSGAIIAGVSRTPVAPLETTIRTHLMVSSGSDSMAGVPRIMRTGMPGLFRGN 180
Qy 181 AVNVLRAVPSKAIIEHFTYDTAKKYLTPPEAGEPKVPITPPLVAGALAGVASTLCTYPMEL 240
Db 181 AVNVLRAVPSKAIIEHFTYDTAKKYLTPPEAGEPKVPITPPLVAGALAGVASTLCTYPMEL 240
Qy 241 VKTRLITEKOVYDNLHAFVKIYRDEBGPGLYRGLAPSLIGVVPYAAANFYAETLRGVY 300
Db 241 VKTRLITEKOVYDNLHAFVKIYRDEBGPGLYRGLAPSLIGVVPYAAANFYAETLRGVY 300
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Db 301 RRASGKEEVGNVPTLLIGSAAAGIASTATPPELVARKOMOVGAVGRQVYKNVLAHMYCI 360
Qy 361 LEKEGTAGLYRGIGSPSCIKLMPAAGISFMCYBCKKILVDEKEDGGAABEQEETETGOAG 420
Db 361 LEKEGTAGLYRGIGSPSCIKLMPAAGISFMCYBCKKILVDEKEDGGAABEQEETETGOAG 420
Qy 421 GOAAPKSSNGDRP 433
Db 421 GOAAPKSSNGDRP 433

RESULT 2

US-10-659-199-18
; Sequence 18, Application US/10659199
; Publication No. US20040038287A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafaleki, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BB1157 US CIP
; CURRENT APPLICATION NUMBER: US/10/659, 199
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/796, 766
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 433
; TYPE: PRN
; ORGANISM: Triticum aestivum
US-10-659-199-18

Query Match 100.0%; Score 2217; DB 15; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.7e-193;

Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 PHLRIVSGAIIAGVSRTPVAPLETTIRTHLMVSSGSDSMAGVPRIMRTGMPGLFRGN 180
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Db 181 AVNVLRAVPSKAIIEHFTYDTAKKYLTPPEAGEPKVPITPPLVAGALAGVASTLCTYPMEL 240

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Qy 241 VKTRLITEKOVYDNLHAFVKIYRDEBGPGLYRGLAPSLIGVVPYAAANFYAETLRGVY 300
Db 241 VKTRLITEKOVYDNLHAFVKIYRDEBGPGLYRGLAPSLIGVVPYAAANFYAETLRGVY 300
Qy 301 RRASGKEEVGNVPTLLIGSAAAGIASTATPPELVARKOMOVGAVGRQVYKNVLAHMYCI 360
Db 301 RRASGKEEVGNVPTLLIGSAAAGIASTATPPELVARKOMOVGAVGRQVYKNVLAHMYCI 360
Qy 361 LEKEGTAGLYRGIGSPSCIKLMPAAGISFMCYBCKKILVDEKEDGGAABEQEETETGOAG 420
Db 361 LEKEGTAGLYRGIGSPSCIKLMPAAGISFMCYBCKKILVDEKEDGGAABEQEETETGOAG 420
Qy 421 GOAAPKSSNGDRP 433
Db 421 GOAAPKSSNGDRP 433

RESULT 3

US-10-425-114-53253
; Sequence 53253, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425, 114
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 53253
; LENGTH: 440
; TYPE: PRN
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: 700802849_FLI pep
US-10-425-114-53253

Query Match 69.0%; Score 1529; DB 15; Length 440;

Best Local Similarity 70.7%; Pred. No. 1.1e-130;

Matches 316; Conservative 37; Mismatches 54; Indels 40; Gaps 9;

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Db 2 MAAAMAATTWYTKNNRASLVMDKKWLLRPVEVAFPMWSQPSRS--LDFPRRALFASV 58
Qy 59 SLSHGAPP--VAREHDK--ARPAD--DYAHQLAA-----GBAGVQXQKAK 102
Db 59 SLSHGAPP--VAREHDK--ARPAD--DYAHQLAA-----GBAGVQXQKAK 102
Qy 103 KAKKQO-----LSIRKVRXIGNPHLRIVSGAIIAGVSRTPVAPLETTIRTHLMVSSGAD 158
Db 103 KAKKQO-----LSIRKVRXIGNPHLRIVSGAIIAGVSRTPVAPLETTIRTHLMVSSGAD 158
Qy 159 SMAGVPRIMRTGMPGLFRGNVNVLRVAPSKAIEHFTYDTAKKYLTPPEAGEPKVPITP 218
Db 159 SMAGVPRIMRTGMPGLFRGNVNVLRVAPSKAIEHFTYDTAKKYLTPPEAGEPKVPITP 218
Qy 219 TPLVAGALAGVASTLCTYPMELVYKTRLTTEKDYDNLHAFVKIYRDEBGPGLYRGLAPS 278
Db 219 TPLVAGALAGVASTLCTYPMELVYKTRLTTEKDYDNLHAFVKIYRDEBGPGLYRGLAPS 278
Qy 234 TPLVAGALAGVASTLCTYPMELIKITVTTEKDYDNLHAFVKIYRDEBGPGLYRGLAPS 293
Db 234 TPLVAGALAGVASTLCTYPMELIKITVTTEKDYDNLHAFVKIYRDEBGPGLYRGLAPS 293
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Db 279 LIGVVPYAAANFYAETLRGVARRASGK-----EVGNVPTLLIGSAAAGIASTATPPL 335
Qy 294 LIGVVPYAAANFYAETLRGVARRASGK-----EVGNVPTLLIGSAAAGIASTATPPL 353
Db 294 LIGVVPYAAANFYAETLRGVARRASGK-----EVGNVPTLLIGSAAAGIASTATPPL 353
Qy 336 RKQMVGAVGROVYKNVLAHMYCIIEKEGTAGLYRGIGSPSCIKLMPAAGISFMCYBCK 395
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Db      414 KILVDEKED-----EEEBDAGGGE 433

RESULT 4
US-10-425-114-50902
; Sequence 50902, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 50902
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3061-107-H7_F11.pcp
US-10-425-114-50902

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Query Match      68.6%; Score 1521.5; DB 15; Length 439;
Best Local Similarity 70.9%; Pred. No. 5,4e-130;
Matches 316; Conservative 38; Mismatches 53; Indels 39; Gaps 10;

Qy      1 MAAAAATMTMKNNRASLVMDKMWLRPEVEVAPPMSSQ--PESRSLDPPRRALPASVG 59
Db      2 MAATAVTTMTWRS-----KESWSLSQVPAVAFPMKPRGKTGGLFPRRAMPASVG 53
Qy      60 LSLSHGAPP--VAREHDK-ARPAD--DVHQQLAA-----GEAGVOKAQKAKK 103
Db      54 LNVCGVAGRDRPRRPPDVRAADNCDIARQLGAAPGQAAMEEBAARRKQGGG 113
Qy      104 AKKQ-----LSLRKRVKIGNPHLRRLVSGAAGAVSRTFVAPLETIRTHLWVGSGADS 159
Db      114 SKKQQLDGLSLRKRVKIANPRLRLVSGAAGAVSRTFVAPLETIRTHLWVGSGADS 173
Qy      160 MAGVFRWIMRTGSGGLPRGNVNVLRVAPSKAIEHFTYDTAKKYLTPRAGSPAKVPIPT 219
Db      174 MAGVQMTQNGMGWGLPRGNVNVLRVAPSKAIEHFTYDTAKKYLTPRAGSPAKVPIPT 233
Qy      220 PLVAGALGAVASTLCTYPMELVKTRLTEKDYDNLHAFKIVRDEGSGELYRGLAPSL 279
Db      234 PLVAGALGAFSTLCTYPMELIKTRVTEKDYDVAHAHFAVILNDEGSELYRGLTPEL 293
Qy      280 IGVVYAAANFYAYETLKGVRASGKE---EVGNVPTLLIGSAGAIASATPPEVAR 336
Db      294 IGVVYAAANFYAYETLKLRYRATGRRGADVGPATLLIGSAGAIASATPPEVAR 353
Qy      337 KOMVGAVGGROVYKQVNHAMCIIEKSTAGLYNGLSCTIKLMPAGISMCYEAACK 396
Db      354 KOMVGAVGGROVYKQVNHAIYCIILKKGAGGLYRGLSPSCIKLMPAGIAFMCEACK 413
Qy      397 ILVDEKEDGGAAPQEBETETGOAGGQ 422
Db      414 ILVDEKED-----EEEBDAG--GGE 432

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RESULT 5
 US-10-425-114-65995
 ; Sequence 65995, Application US/10425114

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; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 65995
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3898-016-B4_F11.pcp
US-10-425-114-65995

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Query Match      68.6%; Score 1521.5; DB 15; Length 439;
Best Local Similarity 70.9%; Pred. No. 5,4e-130;
Matches 316; Conservative 38; Mismatches 53; Indels 39; Gaps 10;

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Db      2 MAATAVTTMTWRS-----KESWSLSQVPAVAFPMKPRGKTGGLFPRRAMPASVG 53
Qy      60 LSLSHGAPP--VAREHDK-ARPAD--DVHQQLAA-----GEAGVOKAQKAKK 103
Db      54 LNVCGVAGRDRPRRPPDVRAADNCDIARQLGAAPGQAAMEEBAARRKQGGG 113
Qy      104 AKKQ-----LSLRKRVKIGNPHLRRLVSGAAGAVSRTFVAPLETIRTHLWVGSGADS 159
Db      114 SKKQQLDGLSLRKRVKIANPRLRLVSGAAGAVSRTFVAPLETIRTHLWVGSGADS 173
Qy      160 MAGVFRWIMRTGSGGLPRGNVNVLRVAPSKAIEHFTYDTAKKYLTPRAGSPAKVPIPT 219
Db      174 MAGVQMTQNGMGWGLPRGNVNVLRVAPSKAIEHFTYDTAKKYLTPRAGSPAKVPIPT 233
Qy      220 PLVAGALGAVASTLCTYPMELVKTRLTEKDYDNLHAFKIVRDEGSGELYRGLAPSL 279
Db      234 PLVAGALGAFSTLCTYPMELIKTRVTEKDYDVAHAHFAVILNDEGSELYRGLTPEL 293
Qy      280 IGVVYAAANFYAYETLKGVRASGKE---EVGNVPTLLIGSAGAIASATPPEVAR 336
Db      294 IGVVYAAANFYAYETLKLRYRATGRRGADVGPATLLIGSAGAIASATPPEVAR 353
Qy      337 KOMVGAVGGROVYKQVNHAMCIIEKSTAGLYNGLSCTIKLMPAGISMCYEAACK 396
Db      354 KOMVGAVGGROVYKQVNHAIYCIILKKGAGGLYRGLSPSCIKLMPAGIAFMCEACK 413
Qy      397 ILVDEKEDGGAAPQEBETETGOAGGQ 422
Db      414 ILVDEKED-----EEEBDAG--GGE 432

```

RESULT 6
 US-10-437-963-150460
 ; Sequence 150460, Application US/10437963
 ; Publication No. US2004012343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

```
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 150460
; LENGTH: 414
; TYPE: PRF
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(414)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_50695C.1.pcp
US-10-437-963-150460

Query Match      66.3%; Score 1470.5; DB 16; Length 414;
Best Local Similarity 72.2%; Pred. No. 2,2e-125;
Matches 314; Conservative 21; Mismatches 55; Indels 45; Gaps 9;

QY 1 MAAMAATTWTTKNNR-----ASLYMDKKNNLLRPVPEVAPWSSQ-----QPESSLDPP 50
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MAAMAAVTTWTRNNAVGGA VAVVDRKGMF--VPEVSPFWSSVEGERINSSSKLFFP 57
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 51 RRA-----LPAVGLSLSHGAPPVAREHDKARPADVAHQOLAA--AGEAGVOKAKAK-K 103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 58 RRTAAPPLFASVGLSLPSAA-----KGRDNCVDARQOLAAAEAEAAKKGKQKMK 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 104 AKKQQLSLRKVRKVGKGNPHLRLVSGA IAGAVSRTFVAPLETTIRTHLMVSSGADSMAGV 163
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 109 GGGGLSLRLKRVKRVKIGNPHLRLLVSGA IAGAVSRTFVAPLETTIRTHLMVSSCGASMAEV 168
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 164 FRMTMREGMPGLFRGNAVNVLRVAPSKAIEHFTYDPAKKYLTPEAGEPAKVPITPTVA 223
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 169 FRMTMREGMTGLFRGNAVNA-----FYDTPAKKYLTPEDDEPAKIPITPVLA 217
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 224 GALAGVASTLCYPMELVKTRLTIEKDVNLLHAFVKIVRDEGPGELVYGLAPSLIGV 283
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 GALAGVASTLCYPMELVKTRLTIEKDVNLLHAFVKIVRDEGPGELVYGLAPSLIGV 277
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 284 PYAANFAYETLRGVYRRASGKEEVNPTLLIGSAGAIASATATPELVARQOMQVGA 343
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 PYATNFAYETLRRLYRRATGRADVGPATLLIGSAGAIASATATPELVARQOMQVGA 337
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 344 VGGROYVKNVLMHMYCILEKEGTAGLYRGIGPSCIKMPAAGISFMCYEACKILVDEKE 403
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 338 VGGROYVKNVLMHMYCILEKEGTAGLYRGIGPSCIKMPAAGISFMCYEALKKVLYVEE- 396
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 404 DGAABPOEETETGQ 418
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 397 ----AAPELAECAE 407
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-09-796-766-21
; Sequence 21, Application US/09796766
; Patent NO. US20010047523A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafaleki, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BB1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
```

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; SOFTWARE: Microsoft Office 97
; SEQ ID NO 21
; LENGTH: 436
; TYPE: PRF
; ORGANISM: Zea mays
US-09-796-766-21

Query Match      63.2%; Score 1401.5; DB 9; Length 436;
Best Local Similarity 65.4%; Pred. No. 4.8e-119;
Matches 291; Conservative 46; Mismatches 69; Indels 39; Gaps 9;

QY 1 MAAMAATTWTTKNNRNASLYMDKKNNLLRPVPEVAPWSSQ-----PESLSLDPFRALPASVG 59
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MAATMAVTTWTRRS-----KESWSSIQVPAVAPPMKRGGKTGGLFEPFRAMPASVG 52
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 60 LSLSHGAPP--VAREHDK-ARPAD--DVNHOAAAGGAGVQAKAKKXQQLSLRKV 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 LNVCPGVAPGRDREDDPKVVRADNCDIAPSLAPPFGSRPPGKRGSGSEEAAGRRH 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 115 RVKIG-----NPHLRRLVSGA IAGAVSRTFVAPLETTIRTHLMVSSGADSM 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 EEAAGRSRSEBEGGQODQPARLVSGA IAGAVSRTFVAPLETTIRTHLMVSSIGVDSM 172
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 161 AGVFRIMRTGMPGLFRGNAVNVLRVAPSKAIEHFTYDPAKKYLTPEAGEPAKVPITPT 220
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 AGVFQWIMQWEGMTGLFRGNAVNVLRVAPSKAIEHFTYDPAKKFLTPKGDDEPKIPITPT 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 221 LVAGALAGVASTLCYPMELVKTRLTIEKDVNLLHAFVKIVRDEGPGELVYGLAPSLI 280
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 LVAGALAGVASTLCYPMELVKTRLTIEKDVNLLHAFVKILRDGSELVYGLPSLI 292
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 281 GVVPYAANFAYETLRGVYRRASGKE---EVGNVPTLLIGSAGAIASATATPELVARQ 337
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 293 GVVPYAANCFYATETLRLYRRATGRAPGADVGPATLLIGSAGAIASATATPELVARQ 352
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 338 QMOVGA VGGROYVKNVLMHMYCILEKEGTAGLYRGIGPSCIKMPAAGISFMCYEACKI 397
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 353 QMOVGA VGGROYVKNVLMHMYCILEKEGTAGLYRGIGPSCIKMPAAGIAFMCYEACKI 412
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 398 LVDEKEDGGAABPOEETETGQAAGQ 422
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 413 LVDEKED-----EEEDGAG--GGE 429
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-10-659-199-21
; Sequence 21, Application US/10659199
; Publication NO. US20040038287A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafaleki, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BB1157 US CIP
; CURRENT APPLICATION NUMBER: US/10/659,199
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/796,766
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 21
; LENGTH: 436
; TYPE: PRF
; ORGANISM: Zea mays
US-10-659-199-21

Query Match      63.2%; Score 1401.5; DB 15; Length 436;
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Best Local Similarity 65.4%; Pred. No. 4,8e-119;
Matches 291; Conservative 46; Mismatches 69; Indels 39; Gaps 9;

QY 1 MAAAAATTMTTKNNRSLVMDKK-NMLLRPVPEVAFPMSSQ--PESISLPPRRALPASVG 59
DB 1 MAAATVMTVTRS-----KESWSIQVPVAFPMKPRGKTGGLFPRRAMPASVG 52
QY 60 LSLSHGAPP--VAREHDK-ARPAD--DVAAHQLAAAGEAGVQKAKKAKKQOLSLRKV 114
DB 53 LNVCGVPAARDPRRPRVRAADNCDLAASLAPFPSPGRPGRCGRSEEEAAGRHH 112
QY 115 RVKIG-----NPHLRRLVSGAIVAGVSRTPVAPLETTIRTHLMVSSGADM 160
DB 113 EBAAGRSEPEEGQODRQPARLVSGAIVAGVSRTPVAPLETTIRTHLMVSGADM 172
QY 161 AGVPMIMTEGMPGLFRGNANVNLRVASKAIEHTYDTAKKYLTPREGPAKVP 220
DB 173 AGVPMIMTEGMPGLFRGNANVNLRVASKAIEHTYDTAKKYLTPREGPAKVP 232
QY 221 LVAGALAGVASTLCYPMELVKTRLTEKOVYDNLLHAFVKIYRDGPGELYRGLAPSL 280
DB 233 LVAGALAGVASTLCYPMELVKTRLTEKOVYDNLLHAFVKIYRDGPGELYRGLAPSL 292
QY 281 GVVPAANFVAYETLRGVYRRASGKE---EVGNVPTLLIGSAGAIASATFPLEVARK 337
DB 293 GVVPAANFVAYETLRGVYRRASGKE---EVGNVPTLLIGSAGAIASATFPLEVARK 352
QY 338 QMVGAVGROYKRVKVLHAMCYCLEKEGTAGLYRGSGSCIKLMPAAGISFMCYACKKI 397
DB 353 QMVGAVGROYKRVKVLHAMCYCLEKEGTAGLYRGSGSCIKLMPAAGISFMCYACKKI 412
QY 398 LVDEKEDGGAEPQETETGQAGGQ 422
DB 413 LVDEKEDGGAEPQETETGQAGGQ 429

RESULT 9
US-10-437-963-146611
; Sequence 146611, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 146611
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_47219C.1.pep
US-10-437-963-146611

Query Match 60.0%; Score 1329.5; DB 16; Length 423;
Best Local Similarity 64.4%; Pred. No. 1.7e-112;
Matches 275; Conservative 47; Mismatches 76; Indels 29; Gaps 8;

QY 1 MAAAAATTMTTKNNRSLVMDKK-NMLLRPVPEVAFPMSSQ--SRLSD---FPRRA 53
DB 1 MAAATVMTVTRS-----KESWSIQVPVAFPMKPRGKTGGLFPRRAMPASVG 52
QY 54 LFASVGLSLSHGAPPV---REHDKARPADVAHQLAA-----GEAGVQK 97
DB 1 MAAATVMTVTRS-----KESWSIQVPVAFPMKPRGKTGGLFPRRAMPASVG 52

DB 59 LFASVGLKVTAPAPVAPSPADHDKIPADHCIRKVVSSAVGVQVPGTEASVNEBEVVD 118
QY 98 AQKAKKAKKQOLSLRKVRKYGKIPHLRLVSGAIVAGVSRTPVAPLETTIRTHLMVSSGA 157
DB 119 GKAATKAKKRGGL--KLKIKIPHLRLVSGAIVAGVSRTPVAPLETTIRTHLMVSSG- 174
QY 158 DSMAGVFRIMTEGMPGLFRGNANVNLRVASKAIEHTYDTAKKYLTPREGPAKVP 217
DB 175 DSMTEVFOSIMTEGMPGLFRGNANVNLRVASKAIEHTYDTAKKYLTPREGPAKVP 234
QY 218 PTPVLVAGALAGVASTLCYPMELVKTRLTEKOVYDNLLHAFVKIYRDGPGELYRGLAP 277
DB 235 PPSLVLGALAGVASTLCYPMELVKTRLTEKOVYDNLLHAFVKIYRDGPGELYRGLAP 294
QY 278 SLIGVPAANFVAYETLRGVYRRASGKEVGNVPTLLIGSAGAIASATFPLEVARK 337
DB 295 SLIGVPAANFVAYETLRGVYRRASGKEVGNVPTLLIGSAGAIASATFPLEVARK 354
QY 338 QMVGAVGROYKRVKVLHAMCYCLEKEGTAGLYRGSGSCIKLMPAAGISFMCYACKKI 397
DB 355 QMVGAVGROYKRVKVLHAMCYCLEKEGTAGLYRGSGSCIKLMPAAGISFMCYACKKI 414
QY 398 LVDEKED 404
DB 415 LVDEKED 421

RESULT 10
US-10-425-114-63026
; Sequence 63026, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63026
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73089B03_FLI.pep
US-10-425-114-63026

Query Match 59.1%; Score 1310; DB 15; Length 444;
Best Local Similarity 65.3%; Pred. No. 1.1e-110;
Matches 278; Conservative 48; Mismatches 70; Indels 30; Gaps 11;

QY 1 MAAAAATTMTTKNNRSLVMDKK-NMLLRPVPEVAFPMSSQ--SRLSD---FPRRA 53
DB 25 MAAATVMTVTRS-----KESWSIQVPVAFPMKPRGKTGGLFPRRAMPASVG 52
QY 54 LFASVGLSLSHGAPPV---REHDKARPADVAHQLAAAGEAGVQK--Q 99
DB 82 LFASVGLKVTAPAPVAPSPADHDKIPADHCKR-VYSEAGVQVISTEASVBEVVD 140
QY 100 KAKK-AKKQOLSLRKVRKYGKIPHLRLVSGAIVAGVSRTPVAPLETTIRTHLMVSSGAD 158
DB 141 KAKKAKKRGGL--KLKIKIPHLRLVSGAIVAGVSRTPVAPLETTIRTHLMVSSG- 196
QY 159 DSMAGVFRIMTEGMPGLFRGNANVNLRVASKAIEHTYDTAKKYLTPREGPAKVP 218
DB 197 SMTEVFOSIMTEGMPGLFRGNANVNLRVASKAIEHTYDTAKKYLTPREGPAKVP 256
QY 219 TPLVAGALAGVASTLCYPMELVKTRLTEKOVYDNLLHAFVKIYRDGPGELYRGLAP 278

Db 257 PSLLAGALAGVSSLTCTYPMELVTRLTIEKDVYNNFLHAFVKILREBGESELYRGILTPS 316
Qy 279 LIGVVPYAAANFYAETLRGVYRRASGKEEVGNVPTLLIGSAGAIATAFPLEVARKQ 338
Db 317 LIGVVPYAAANFYAYDTLTKLYRKTFFKQEISNATLILIGSAGAIATAFPLEVARKQ 376
Qy 339 MOVGAVGROVYKVVLAHMYCILEKEGTAGLYRGILGPSICILMPAAGISFVCEACKKIL 398
Db 377 MOVGAVGROVYKVVLFALYCIIMEKEGVGLYKGLGPSICILMPAAGISFVCEACKKIL 436
Qy 399 VDEKED 404
Db 437 VEDNED 442

RESULT 11

US-10-425-114-63935
; Sequence 63935, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingtong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63935
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4738-065-E6_FLI.pep
US-10-425-114-63935

Query Match 59.1%; Score 1310; DB 15; Length 444;
Best Local Similarity 65.3%; Pred. No. 1.1e-110;
Matches 278; Conservative 48; Mismatches 70; Indels 30; Gaps 11;

Qy 1 MAAMAATTMTWTKNNRSLVMDKK-NMLRFPVPEVAPFMSQPE---SRSLDF---PRRA 53
Db 25 MAAMVAMTARSKN-SILPMEKQGSIQ-LPELRFPWDSHEDKGFSLQSQSPSHG 81
Qy 54 LFASVGLSLSHGAPVA-----REHDKARPADVAHQLAAGEAGVOKA--Q 99
Db 82 LFASVGLKSTGAFAVAPGPDKDIKLPFDHCKM-KVSEAVGVQVISTEASEVEVDA 140
Qy 100 KAKK-AKKQOISLRKRVKIGNPHLRVSGAIGAVSRFTVADLETIRTHLMYSSGAD 158
Db 141 KAKKAARKRGQL---KIKIGNPHLRVSGAIGAVSRFTVADLETIRTHLMYSSNG-D 196
Qy 159 SMAGVPEMIMTEGMPGLFRGNLVNVRVAPSKAIEHFTYDTAKKYLTPREGEPAKYP 218
Db 197 SMTEVFOSIMTEGMPGLFRGNLVNVRVAPSKAIEHFTYDTAKKYLTPREGEPAKYP 256
Qy 219 TPLVAGALAGVASTLCTYPMELVTRLTIEKDVYNNFLHAFVKILREBGESELYRGILAPS 278
Db 257 PSLLAGALAGVSSLTCTYPMELVTRLTIEKDVYNNFLHAFVKILREBGESELYRGILTPS 316
Qy 279 LIGVVPYAAANFYAETLRGVYRRASGKEEVGNVPTLLIGSAGAIATAFPLEVARKQ 338
Db 317 LIGVVPYAAANFYAYDTLTKLYRKTFFKQEISNATLILIGSAGAIATAFPLEVARKQ 376
Qy 339 MOVGAVGROVYKVVLAHMYCILEKEGTAGLYRGILGPSICILMPAAGISFVCEACKKIL 398
Db 377 MOVGAVGROVYKVVLFALYCIIMEKEGVGLYKGLGPSICILMPAAGISFVCEACKKIL 436

Qy 399 VDEKED 404
Db 437 VEDNED 442

RESULT 12

US-10-425-114-52078
; Sequence 52078, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingtong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 52078
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700093540_FLI.pep
US-10-425-114-52078

Query Match 59.0%; Score 1309; DB 15; Length 444;
Best Local Similarity 65.2%; Pred. No. 1.4e-110;
Matches 277; Conservative 47; Mismatches 73; Indels 28; Gaps 10;

Qy 1 MAAMAATTMTWTKNNRSLVMDKK-NMLRFPVPEVAPFMSQPE---SRSLDF---PRRL 54
Db 25 MAAMVAMTARSKNSILP-VEKQGSIQ-LPELRFPWDSHEDKGFSLQSQSPSHGL 82
Qy 55 FASVGLSLSHGAPVA-----REHDKARPADVAHQLAAGEAGVOKA--QK 100
Db 83 FASVGLKSTGAFAVAPGPDKDIKLPFDHCKMYP-EAVGVQVISTEASEVEVDAK 141
Qy 101 AKK-AKKQOISLRKRVKIGNPHLRVSGAIGAVSRFTVADLETIRTHLMYSSGADS 159
Db 142 AKKAARKRGQL---KIKIGNPHLRVSGAIGAVSRFTVADLETIRTHLMYSSNG-DS 197
Qy 160 MAGVPEMIMTEGMPGLFRGNLVNVRVAPSKAIEHFTYDTAKKYLTPREGEPAKYP 219
Db 198 MTEVFOSIMTEGMPGLFRGNLVNVRVAPSKAIEHFTYDTAKKYLTPREGEPAKYP 257
Qy 220 PLVAGALAGVASTLCTYPMELVTRLTIEKDVYNNFLHAFVKILREBGESELYRGILAPS 279
Db 258 SLTAGALAGVSSLTCTYPMELVTRLTIEKDVYNNFLHAFVKILREBGESELYRGILTPS 317
Qy 280 IGVPYAAANFYAETLRGVYRRASGKEEVGNVPTLLIGSAGAIATAFPLEVARKQ 339
Db 318 IGVPYAAANFYAYDTLTKLYRKTFFKQEISNATLILIGSAGAIATAFPLEVARKQ 377
Qy 340 QVAVGROVYKVVLAHMYCILEKEGTAGLYRGILGPSICILMPAAGISFVCEACKKIL 399
Db 378 QVAVGROVYKVVLFALYCIIMEKEGVGLYKGLGPSICILMPAAGISFVCEACKKIL 437
Qy 400 DEKED 404
Db 438 EDNED 442

RESULT 13

US-10-437-963-122416
; Sequence 122416, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

Query Match	53.8%	Score 1193	DB 16	Length 415
Best Local Similarity	65.3%	Pred. No. 6e-100		
Matches 225	Conservative 47	Mismatches 72	Indels 6	Gaps 2

RESULT 14
US-10-425-114-67044

```

? APPLICANT: Liu, Jingdong
? APPLICANT: Zhou, Yihua
? APPLICANT: Kovalic, David K.
? APPLICANT: Screen, Steven E.
? APPLICANT: Tabaska, Jack E
? APPLICANT: Cao, Yongwei
? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
? FILE REFERENCE: 38-21(5313)B
? CURRENT APPLICATION NUMBER: US/10/425,114
? CURRENT FILING DATE: 2003-04-28
? NUMBER OF SEQ ID NOS: 73128
? SEQ ID NO 67044
? LENGTH: 431

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; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: clone ID: LIB4757-025-G11_FLI.pep

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Query Match	51.9%;	Score 1151.5;	DB 15;	Length 431;
Best Local Similarity	63.8%;	Pred. No. 3.2e-96;		
Matches 229;	Conservative 49;	Mismatches 72;	Indels 9;	Gaps 3;

RESULT 15

; patent No. US20010047523A1
; GENERAL INFORMATION:

APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: BRITISH-1 HOMOLOGS

FILE REFERENCE: BB157 US CIP

;
CURRENT FILING DATE: 2001-03-01
;
CURRENT APPLICATION NUMBER: US/09/

;
; PRIOR APPLICATION NUMBER: 09/
; PRIOR FILING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: PCT/US99/06583
PRIOR FILING DATE: 1999-03-22

PRIOR APPLICATION NUMBER: 60/079420

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; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21

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; SOFTWARE: Microsoft Office 97
; SEO ID NO 20

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LENGTH: 289

ORGANISM: Triticum aestivum

US-09-796-766-20

Query Match	51.4%;	Score 1139.5;	DB 9;	Length 289;
Best [local] Similarity	74.5%;	Pred. No. 2,2e-95;		

Matches 216; Conservative 37; Mismatches 36; Indels 1; Gaps 1;

115 RYKGNPHLRRLVSGAIAGAVSRTPVAPLETIRTHLMVSSGADSMAGVFRWIMRTEGWP 17

Db
1 KIKVGNHLKRLISGGIAGAVSRITVAPLETIRTHLMVGSNG-NSSTEVPDSIMKNEGWT 59

175 GLEFGNAVNVLRYAPSKAIEHETVDTAKKYLTPPEAGBPAYPIPTPLVAGALAGVASTLC 23

[illegible][illegible]

235 TYPMELVKRLTIKDWYDNLHAFKIVRDEGPGEYRGLAPSLIGVPPAAANFYAYE 29

Db 120 TYPELIKTRLTQGVYDNFLHAFVKIVREEGPAELYRGLTPSLIGVVPYAATNYFAYD 175

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OM protein - protein search, using sw model

Run on: May 25, 2005, 12:31:55 ; Search time 222 Seconds
(without alignments)
145.599 Million cell updates/sec

Title: US-10-659-199-18

Perfect score: 2217
Sequence: 1 MAAAMAATTMTKNNRASLV.....TETGAGGQAPKSSNGDRP 433

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2217	100.0	433	4 US-09-796-766-18	Sequence 18, Appl
2	1401.5	63.2	436	4 US-09-796-766-21	Sequence 21, Appl
3	1139.5	51.4	289	4 US-09-796-766-20	Sequence 20, Appl
4	1001	45.2	272	4 US-09-796-766-14	Sequence 14, Appl
5	589.5	26.6	410	4 US-09-796-766-10	Sequence 10, Appl
6	463	20.9	252	4 US-09-796-766-4	Sequence 4, Appl
7	459	20.7	109	4 US-09-796-766-16	Sequence 16, Appl
8	425.5	19.2	469	3 US-09-188-930-339	Sequence 339, App
9	425.5	19.2	469	4 US-09-312-283C-339	Sequence 339, App
10	401.5	18.1	180	4 US-09-796-766-8	Sequence 8, Appl
11	355.5	16.0	320	2 US-08-933-750C-12	Sequence 12, Appl
12	355.5	16.0	320	3 US-09-234-613-12	Sequence 12, Appl
13	355.5	16.0	320	4 US-09-976-594-711	Sequence 711, App
14	355	16.0	269	4 US-09-248-796A-117733	Sequence 20733, A
15	348	15.7	685	4 US-09-949-016-11180	Sequence 11180, A
16	345	15.6	678	4 US-09-949-016-6406	Sequence 6406, Ap
17	341	15.4	447	4 US-09-160-119-4	Sequence 2, Appl
18	332	15.0	674	3 US-09-160-119-2	Sequence 2, Appl
19	318	14.3	227	4 US-09-248-796A-20731	Sequence 20731, A
20	314.5	14.2	301	4 US-09-270-767-32789	Sequence 32789, A
21	314.5	14.2	227	4 US-09-270-767-48006	Sequence 48006, A
22	305.5	13.8	328	3 US-09-068-140A-15	Sequence 10, Appl
23	305.5	13.8	328	3 US-09-068-140A-15	Sequence 10, Appl
24	277.5	12.5	306	4 US-09-248-796A-117738	Sequence 11738, A
25	276.5	12.5	76	4 US-09-796-766-12	Sequence 12, Appl
26	272.5	12.3	302	4 US-09-270-767-33858	Sequence 33858, A
27	272.5	12.3	302	4 US-09-270-767-49075	Sequence 49075, A

28	271.5	12.2	358	4 US-09-270-767-44738	Sequence 44738, A
29	267	12.0	307	4 US-09-248-796A-17597	Sequence 17597, A
30	265	12.0	260	4 US-09-270-767-44590	Sequence 44590, A
31	263	11.9	301	4 US-09-949-016-6865	Sequence 6865, Ap
32	263	11.9	298	4 US-09-949-016-9952	Sequence 9952, Ap
33	260	11.7	338	3 US-08-961-871-10	Sequence 47, Appl
34	258.5	11.7	297	4 US-09-434-354-47	Sequence 47, Appl
35	258.5	11.7	297	4 US-09-709-785-47	Sequence 47, Appl
36	256	11.5	365	4 US-09-270-767-43637	Sequence 43637, A
37	255	11.5	293	4 US-09-248-796A-17601	Sequence 17601, A
38	255	11.5	304	4 US-09-949-016-11339	Sequence 11339, A
39	250	11.3	298	4 US-09-434-354-49	Sequence 49, Appl
40	250	11.3	298	4 US-09-709-785-49	Sequence 49, Appl
41	245.5	11.1	381	4 US-09-248-796A-15499	Sequence 15499, A
42	244.5	11.0	299	4 US-09-248-796A-17636	Sequence 17636, A
43	243	11.0	112	4 US-09-796-766-2	Sequence 2, Appl
44	243	11.0	351	2 US-08-933-750C-19	Sequence 19, Appl
45	243	11.0	351	3 US-09-234-613-19	Sequence 19, Appl

ALIGNMENTS

```

RESULT 1
US-09-796-766-18
; Sequence 18, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: B1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; PRIOR APPLICATION NUMBER: 2001-03-01
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-796-766-18

Query Match      100.0%; Score 2217; DB 4; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.2e-223;
Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAAAMAATTMTKNNRASLVMDKQMLRPVEVAFPMSSQPSRLDPFRRLFPASVGL 60
1 MAAAMAATTMTKNNRASLVMDKQMLRPVEVAFPMSSQPSRLDPFRRLFPASVGL 60
61 SLSHGAPVAREHDKARPADVAHQLAAGAGVQAKAKAKKQQLSLRVRVYKGN 120
61 SLSHGAPVAREHDKARPADVAHQLAAGAGVQAKAKAKKQQLSLRVRVYKGN 120
61 SLSHGAPVAREHDKARPADVAHQLAAGAGVQAKAKAKKQQLSLRVRVYKGN 120
121 PHLRRLVSGALVAGVSRTPVAPLETIRTLVWGSSGADSMAGVFRIMTEGPGFLFRGN 180
121 PHLRRLVSGALVAGVSRTPVAPLETIRTLVWGSSGADSMAGVFRIMTEGPGFLFRGN 180
121 PHLRRLVSGALVAGVSRTPVAPLETIRTLVWGSSGADSMAGVFRIMTEGPGFLFRGN 180
181 AVNVLKVPASKAIEHFTYDTAKKYLTPKAGBPAKVPFPLVAGALAGVASTLCTPMEL 240
181 AVNVLKVPASKAIEHFTYDTAKKYLTPKAGBPAKVPFPLVAGALAGVASTLCTPMEL 240
181 AVNVLKVPASKAIEHFTYDTAKKYLTPKAGBPAKVPFPLVAGALAGVASTLCTPMEL 240
241 VVTRLRLTEKDVYDNLHAFVKIVRDEGPGELVGLAPSLIGVVPYAAANFVAYETLRGVY 300
241 VVTRLRLTEKDVYDNLHAFVKIVRDEGPGELVGLAPSLIGVVPYAAANFVAYETLRGVY 300
241 VVTRLRLTEKDVYDNLHAFVKIVRDEGPGELVGLAPSLIGVVPYAAANFVAYETLRGVY 300

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QY 301 RRASGKEEVNPTLLIGSAGAIATATPELEVARQOMOVAGSGROYVKNVLAHMYCI 360
| | | | |
DB 301 RRASGKEEVNPTLLIGSAGAIATATPELEVARQOMOVAGSGROYVKNVLAHMYCI 360
QY 361 LEKXGTGLYRGGLPSCIKLMPAAGISFMCYEAACKTILVDEKEDGAAEPOEETETQAG 420
| | | | |
DB 361 LEKXGTGLYRGGLPSCIKLMPAAGISFMCYEAACKTILVDEKEDGAAEPOEETETQAG 420
QY 421 GOAAPKSSNGDRP 433
| | | | |
DB 421 GOAAPKSSNGDRP 433

RESULT 2

US-09-796-766-21
; Sequence 21, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafaleki, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: B1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 21
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Zea mays
US-09-796-766-21

Query Match 63.2%; Score 1401.5; DB 4; Length 436;
Best Local Similarity 65.4%; Pred. No. 6.2e-118;
Matches 291; Conservative 46; Mismatches 69; Indels 39; Gaps 9;

QY 1 MAAMAATTWVTNKNRSLVMDKKWMLRPVEYAFPPSSQ-PPSRSLDEPRRALFASVG 59
| | | | |
DB 1 MAAMAATTWVTNKNRSLVMDKKWMLRPVEYAFPPSSQ-PPSRSLDEPRRALFASVG 59
QY 60 LSLSHGAPP--VAEHDGK--ARPAD--DVAHQLAAGGAGVQAKAKKAKKQQLSRKV 114
| | | | |
DB 53 LNVCPGVAGRPDRPDPKVVRAADNCDIASLAPPPGSRPPGRGRGSEEBEABGRRH 112
QY 115 RVKIG-----NPHLRIVSGAIAAGVSRTPVAPLETTITHLMVSGGSDSM 160
| | | | |
DB 113 EEAAGRSEEBEGQDROPARPARLVSGAIAAGVSRTPVAPLETTITHLMVSGSIIVDSM 172
QY 161 AGVFRWIMRTGMPGLFRGNANVNLRYAPSKAIEHFTYDPAKYLTPPEAGEPAPVPTP 220
| | | | |
DB 173 AGVFRWIMQNBGWTGLFRGNANVNLRYAPSKAIEHFTYDPAKYLTPPEAGEPAPVPTP 232
QY 221 LVAGALGAVASTLCITYPELVTKLTLEKDYDNLHAIFYIVDESGPGLYRGLASLI 280
| | | | |
DB 223 LVAGALGAVASTLCITYPELVTKLTLEKDYDNLHAIFYIVDESGPGLYRGLASLI 292
QY 281 GVVYVYAAANFYAVETLIGVYRASAQK---EVGNVPTLLIGSAGAIATATPELEVAR 337
| | | | |
DB 293 GVVYVYAAANFYAVETLIGVYRASAQK---EVGNVPTLLIGSAGAIATATPELEVAR 352
QY 338 QMOVAGVAGSGROYVKNVLAHMYCILEKGTAGLYRGLPSCIKLMPAAGISFMCYEAACKI 397
| | | | |
DB 353 QMOVAGVAGSGROYVKNVLAHMYCILEKGTAGLYRGLPSCIKLMPAAGISFMCYEAACKI 412
QY 398 LVDEKEDGAAEPOEETETQAGGQ 422
| | | | |

DB 413 LVDEKDE-----EEDEAG--GGE 429

RESULT 3

US-09-796-766-20
; Sequence 20, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafaleki, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: B1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-09-796-766-20

Query Match 51.4%; Score 1139.5; DB 4; Length 289;
Best Local Similarity 74.5%; Pred. No. 9.1e-111;
Matches 216; Conservative 37; Mismatches 36; Indels 1; Gaps 1;

QY 115 RVKIGNPHLRIVSGAIAAGVSRTPVAPLETTITHLMVSGGSDSMAGVFRWIMRTGMP 174
| | | | |
DB 1 KIVGNSHLKRLISGGIAGVSRTPVAPLETTITHLMVSGNSG--NSTEYFDSIMKQEGWT 59
QY 175 GLFRGNANVNLRYAPSKAIEHFTYDPAKYLTPPEAGEPAPVPTPVLVAGALGAVASTLC 234
| | | | |
DB 60 GLFRGNANVNLRYAPSKAIEHFTYDPAKYLTPPEAGEPAPVPTPVLVAGALGAVASTLC 119
QY 235 TYPELVKTLTLEKDYDNLHAIFYIVDESGPGLYRGLASLI GVVYVYAAANFYAYE 294
| | | | |
DB 120 TYPELVKTLTLEKDYDNLHAIFYIVDESGPGLYRGLASLI GVVYVYAAANFYAYE 179
QY 295 TLEGVYRRASGKEEVNPTLLIGSAGAIATATPELEVARQOMOVAGSGROYVKNV 354
| | | | |
DB 180 TLEGVYRRASGKEEVNPTLLIGSAGAIATATPELEVARQOMOVAGSGROYVKNV 239
QY 355 HAMYCILEKGTAGLYRGLPSCIKLMPAAGISFMCYEAACKTILVDEKED 404
| | | | |
DB 240 HALTLIEDGAGVGLYRGLPSCIKLMPAAGISFMCYEAACKTILIEENE 289

RESULT 4
US-09-796-766-14
; Sequence 14, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafaleki, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: B1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21

SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 272
TYPE: PRT
ORGANISM: Glycine max
US-09-796-766-14

Query Match 45.2%; Score 1001; DB 4; Length 272;
Best Local Similarity 71.3%; Pred. No. 2, 7e-96;
Matches 194; Conservative 36; Mismatches 40; Indels 2; Gaps 2;

QY 133 GAVSRTPVAPLETIRTHLMVSSGADSMAGVFRMIMTEGMPGLFRGNANVLRVAPSKA 192
DB 3 GAVSRTPVAPLETIRTHLMVSSGADSMAGVFRMIMTEGMPGLFRGNANVLRVAPSKA 61
QY 193 IEHFTYDTAKVLTPEAGBPAKPIPRPLVAGALAGVASTLCTYPMELVKTRLTIEKDY 252
DB 62 IELPAVDYVKQISPPRGEQPIIPIPSSVAGAVAGVSSSTLCTYPDELTLTRLTIVRGVY 121
QY 253 DNLLHAFVKIVRDEGEGELVRLAPSLIGVFPAAAFVAYETLRGVRASKEEYGNV 312
DB 122 KNLDDAFVRIYVGEPAELVRLAPSLIGVFPAAAFVAYETLRGVRASKEEYGNV 181
QY 313 PTLIGSAGALASTATFPLEVARKQWQVAGVGRQVYKXVLAHMYCILEKEGTAGIYRG 372
DB 182 MTLIGSAGALASTATFPLEVARKQWQVAGVGRQVYKXVLAHMYCILEKEGTAGIYRG 240
QY 373 LGPSCIKLMPADISFMCYACKILVDEKED 404
DB 241 LGPSCIKLMPADISFMCYACKILVDEKED 272

RESULT 5

US-09-796-766-10
Sequence 10, Application US/09796766
Patent No. 6660850
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lightner, Jonathan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
FILE REFERENCE: BB1157 US CIP
CURRENT APPLICATION NUMBER: US/09/796,766
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/668884
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: PCT/US99/06583
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: 60/079420
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 410
TYPE: PRT
ORGANISM: Glycine max
US-09-796-766-10

Query Match 26.6%; Score 589.5; DB 4; Length 410;
Best Local Similarity 40.5%; Pred. No. 6, 5e-53;
Matches 121; Conservative 74; Mismatches 85; Indels 19; Gaps 5;

QY 118 IGNPHLRRLVSGALAGVARTFVAPLETIRTHLMVSSGADSMAGVFRMIMTEGMPGLF 177
DB 107 LGSREVRERISGALSAMTKALAPLETIRTRMVVQ-VSSKNAGSFIEVIEEQGQGLM 165
QY 178 RGNVAVVLRVAPSKAIEHFTYDTAKKYLTP-----EAGBPAKPIPR-----TPL 221
DB 166 AGNMIMMLIVPQALIEGTGFEVCYKRAMSLHEKMSNEYPLQIPIPNINSLSTISV 225
QY 222 -VAGALAGVASTLCTYPMELVKTRLTIEKDYDNLLHAFVKIVRDEGEGELVRLAPSLI 280
DB 226 A1AGNAAAGIASTLVCHPLFVLRDLKRLTVSPSETVPSLGIARNIYKDGQVGAFAVAGISPTLV 285

QY 281 GVVPYAAAFVAYETLRGVYRRASGKEEYGNVPTLIGSAGALASTATFPLEVARKQW 340
DB 286 GMLPYSTCFYEMDTIKESYCRFKSKSLRPEMLLIGALAGTASTISFPLEVARKRLM 345
QY 341 VQAVGROYKXVLAHMYCILEKEGTAGIYRGIGPSCIKLMPADISFMCYACKILV 399
DB 346 VQALQCK-CPPNVAALSEVIREGLKGLYRGWAGACLAKMPSSGITMWFYEAOKDILL 403

RESULT 6

US-09-796-766-4
Sequence 4, Application US/09796766
Patent No. 6660850
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lightner, Jonathan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
FILE REFERENCE: BB1157 US CIP
CURRENT APPLICATION NUMBER: US/09/796,766
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/668884
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: PCT/US99/06583
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: 60/079420
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
LENGTH: 252
TYPE: PRT
ORGANISM: Hordeum vulgare
US-09-796-766-4

Query Match 20.9%; Score 463; DB 4; Length 252;
Best Local Similarity 40.2%; Pred. No. 5, 5e-40;
Matches 99; Conservative 55; Mismatches 74; Indels 18; Gaps 4;

QY 175 GLRGNAVAVVLRVAPSKAIEHFTYDTAKKYLTP-----EAGBPAKPIPR-----AKVPIPTPL- 221
DB 4 GLWVGNTIMIMHILPQALIEGTGFEVYKRGMSAGCKWEDGCPKIQLNMMNIEIRLHL 63
QY 222 ---VAGALAGVASTLCTYPMELVKTRLTIEKDYDNLLHAFVKIVRDEGEGELVRLAP 277
DB 64 SPVALAGAAAGIAGTLMCHPLFVIRKRLTVDRVTYPSISIAFSKIYRTGIRGLYGLCP 123
QY 278 SLIGVFPYAAAFVAYETLRGVYRRASGKEEYGNVPTLIGSAGALASTATFPLEVAR 337
DB 124 TLIGMLPYSTCFYEMDTIKESYCRHLHKKSLSRPELLIIGALVGLTASTISFPLEVAR 183
QY 338 QMVGAVGROYKXVLAHMYCILEKEGTAGIYRGIGPSCIKLMPADISFMCYACKIKI 397
DB 184 RLWVGLQCK-CPPNVAALSEVIREGLKGLYRGWAGACLAKMPSSGITMWFYEAOKD 242
QY 398 LVDEKE 403
DB 243 LLAERD 248

RESULT 7

US-09-796-766-16
Sequence 16, Application US/09796766
Patent No. 6660850
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lightner, Jonathan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
FILE REFERENCE: BB1157 US CIP
CURRENT APPLICATION NUMBER: US/09/796,766
CURRENT FILING DATE: 2001-03-01

Query Match	19.2%	Score 425.5	DB 3	Length 469
Best Local Similarity	29.0%	Pred. 1.12e-35		
Matches 117	Conservative 63	Mismatches 14	Indels 75	Gaps 10

QY	6	AATMTVTKNNRNASLVMDDKNM----	LIRPV----	PEVAFPMSSQPSRSLLDPPRRALFASV	58
Db	119	AEKILSKDDKNGKTWTDIDNEMRWYHLHPVNIPIILYY-----			158
QY	59	GLSLSHGAPVAREHDKCARPADVDVAHOLAAGEGYOAKAKKAKQOLSKRVYKI			118
Db	159	-----KHSFIPIVGEUHLVYPDEFTVEERQTCM-----			185
QY	119	GNPHLRRLVSGAIIAGAVSRTFVAAPLETRITLHMVSSGADSM--AGVPRMTETEGWDL			176
Db	186	---WRRHLVVAQGGAGAAVSRTCAPLDRLKVLMOVAASSNNMCIVGGTQIMIREGAKSL			242
QY	177	FRGNAVNVLRVAPSKAIEHFTYDPAKKYLITPEAGEPAPKVPITPLVAGALGVASTLCTY			236
Db	243	WRGNGINVLKIAPESAIKFMAYVEQMKRLV---GSPDETIRIHERLVAAGSLGALIAQSSIIY			299

Query Match	19.2%	Score 425.5	DB 4	Length 469
Best Local Similarity	29.0%	Pred. No. 1.2e-35		
Matches 117	Conservative	63	Mismatches 149	Indels 75
Gaps				10
QY	6	AATTWTKNNRSLVMDKKW----	LLRPV--	EVAFPMWSQPSRSLDFPRRLASV 58
Db	119	AEKILMSMDKNGTWTITDNNEMRDYHLHPVENIPEILY-----		158
QY	59	GLSLSHGAPPAVREHDGKARPADDYAHQALAAAGVGQKAKKAKKQQLSLKRVKI 118		
Db	159	-----KSTTIFDVGENTVPEDEFTVEERTGM-----		185
QY	119	GNPHLERLVGAIAAGVSRTPFAVPLETIRTLHMVSGSADSM--AGVFRWIMRTGMPGL 1767		
Db	186	---WPHLVAAGGAGAVSRTCTAPIDRLKVLMOQHASSNNMCIVGGTQMIRGCAKSL 2424		
QY	177	FRGNAAVNLVAPSKAIEHFTYDTAKKYLTPBAGPAKVIPTPLVAGALAGVASTLCY 236		
Db	243	WRNGCINVLKIPBSAIFKMAVEQMKRLV--GSPQETLRITHEHLVAGSLAGATAOSS 2399		
QY	237	PHELVNTRLTIEK--DYVGNLLHAFKVIYRDGPGELVGLAPSLIGVPPAAAFVAYET 295		
Db	300	PHEVLKTRALKTKQOYSGMDPCARRILAKEGVAAFYGYIPNNLGIIPYAGIDLAVET 3558		
QY	296	LRCGV--RRASGKEEKGVPFTLLIGSAGAIASATAPLEVARKOMQVA--VGGRGVYK 3511		
Db	360	LKNTWLQRAVAVASADPGVAVLLACGTISSTGQLASVYALVFRRMQQAQASIEGAPETM 419		
QY	352	NVLHAMYCTLEKSGTAGLYRGIGPSCYKLPMPAAGISFMCYACK 355		
Db	420	SSLFFQ--ILTRTEGAFGLYRGILAPFMKVIYAVISLTVVYENLK 461		

RESULT 10
US-09-796-766-8
; Sequence 8, Application US/09796766

```
Patent No. 6660850
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lightner, Jonathan
APPLICANT: Ralski, Antoni
TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
FILE REFERENCE: BB1157 US CIP
CURRENT APPLICATION NUMBER: US/09/796,766
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/668884
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: PCT/US99/06583
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: 60/079420
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Microsoft Office 97
SEQ ID NO 8
LENGTH: 180
TYPE: PRT
ORGANISM: Glycine max
US-09-796-766-8

Query Match      18.1%; Score 401.5; DB 4; Length 180;
Best Local Similarity 44.4%; Pred. No. 9.1e-34;
Matches 79; Conservative 42; Mismatches 56; Indels 1; Gaps 1;

QY 222 VAGALAGVASTLCYTMELVKTRLITEKQVYDNLHAFVKIYRDESGPGLYGLASLIG 281
DB 1 IGAAGAAGIASTLVCHLEVLKDLTVSPETYSIGIAIRNIYDGGVGFAGISPTLVG 60

QY 282 VVPAANFYAYETLRGVRRASGKEVGNVPTLLIGSAAAGIATATPPLVARRKQMV 341
DB 61 MIPYSTCFYFWDTIKESYCRYSKKSLSRPEMLIGALGFTASTISPLEVARRRLNV 120

QY 342 GAVGQGVKNVLYHMYCTIEKEGTAGLYRGLGSPSCIKLMPAAGISFMCYEACKILV 399
DB 121 GALQGR-CPPNMAALSEVIREBGLKGLRGMGASCLXMPSSGITWMTYEAKDILL 177

RESULT 11
US-08-933-750C-12
Sequence 12, Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASCSE0 for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
```

```
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLNOT02
CLONE: 207452
US-08-933-750C-12

Query Match      16.0%; Score 355.5; DB 2; Length 320;
Best Local Similarity 30.3%; Pred. No. 1.5e-28;
Matches 89; Conservative 62; Mismatches 120; Indels 23; Gaps 8;

QY 120 NPHLRVLSGALAGAVSRFTVAPLETIRTHLVWS---SGADSWA---GVF---RWIMRT 170
DB 13 NTKFOYAVAGSVSGVLTTRALISPPDYIKIRFQLOHERLSRSPSAKYHILQASRQILO 72

QY 171 EGMPLFRGNANVNLRVAPSKAIEHFTYDTAKKYLTPPEAGBPAKPIPTPLVAGALAGVA 230
DB 73 BGPATFWKHGVPAQALISIGYAVQFLSFEMLELVARGSVYDAR-BFSVHPFCGGLAACM 131

QY 231 STLCTYEMELVKTRLTI--EKDYDNLHAFVKIYRDESGPGLYRGLASLIGVYVYAA 288
DB 132 ATLTHVPVDVLTTRPAQGEPRVYNTLRRHVGTMVRSBGPQVFKGLATPLTIAIPYAGL 191

QY 289 NFVAYETLRGVYR---RASGKEVGNVPTLLIGSAAAGIATATPPLVARRKQMV--- 342
DB 192 QPSCYSLHLYKMAIPBEGKKN-EYLQWLLCGSGAGVISKTLTYPLDLPKRLQVGGRE 250

QY 343 ---AVGQGVKNVLYHMYCTIEKEGTAGLYRGLGSPSCIKLMPAAGISFMCYE 392
DB 251 HARAAPFGQVRRYKGLMDCAKQVLTQKEGALGFPKGLSPSLTXAALSGFNFPSYE 304

RESULT 12
US-09-234-613-12
Sequence 12, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASCSE0 for Windows Version 2.0
CURRENT APPLICATION DATA:
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RESULT 15
US-09-949-016-11180
; Sequence 11180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11180
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11180

Query Match      15.7%; Score 348; DB 4; Length 685;
Best Local Similarity 27.5%; Pred. No. 2.9e-27;
Matches 106; Conservative 73; Mismatches 163; Indels 44; Gaps 12;

QY      75 GKARPAD-DVAHQLA-----AGE---AGVOK-AQKAKKAKKQOLS--LRKVRKIGNP-- 121
DB      268 GGVTLLEIDILYQLADLVNAGRLTLADIERIAPLAEGALPYNIAELORQSPGLGRPIW 327
QY      122 -----HLRLVSGAIAAGAVSRTFVAPLETIRTHLMVSGSGADSMAG-----VERWI 167
DB      328 LQIAESAYFTLGSVAGAVGATAVYPIDIVKTR-MQNGRSGSVGELMYKNSPDCFKY 386
QY      168 MTEGMPLGFRGNANVNLVAPSKAIEHTYDTAKKYLTPFAGEPAKVPITPPLVAGALA 227
DB      387 LKYEGRFGLYRGLIQLIGVAPEKAIKLVNDFVRDKFTTRDG--SVPLPAEVLGGCA 443
QY      228 GVASTLCTYPMEVLVTRLTIEKDVYDNLHAFVKIVDEGPGLYKGLAPSLIGVVPYA 287
DB      444 GGSQYIFTNPLPLIVIKRLVAGEITTGPRVSALNVLRDGIKGLYKGAACFLRDIPEFA 503
QY      288 ANFVAYETLRGVYRRASGEVGNVPTLLISAGALASTATPPLVARKQMGAVGGR 347
DB      504 IYFPYAHCKLADENG--HVGGLNLAAAGAVPASPVLTPADVIRKRLQVABAGQ 561
QY      348 QYKRVNLHAMYCILEKEGTAGLYRGISPCITLMPAGISPMCYENCKKILVDEKEDGA 407
DB      562 TTYSGVIDCFRKILREEGSPAFWKGTAAVFRSSPOFGVTLVYELLORWFY---IDFGG 618
QY      408 AEPQETETGAGGQAAPKSSNGDRP 433
DB      619 LKP-----AGSEPTPKSRIADLP 636
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Search completed: May 25, 2005, 14:28:39
Job time : 223 secs

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Db      293 GVPYAAACNFYAVETTLKRLYRATGRPRGADVGVATLLIGSAGAIASSATFPLEVARK 352
Qy      338 QMOVGANGROVKNVYHAMVCTLEKEGTGLVYRGVGPSCIKLMPAAGISPMCEACCKI 397
Db      353 QMOVGANGROVKNVYHAMVCTLEKEGTGLVYRGVGPSCIKLMPAAGISPMCEACCKI 412
Qy      398 LVDEKEDGAAEPOEETETGOAGQ 422
Db      413 LVDEKEDS-----EEDEAG--GGE 429

RESULT 2
T01350
adenvylate translocator britle-1 homolog F8B4.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T01350
R:Bevan, M.; Terry, N.; Ardiiles, W.; Buysbaert, C.; Daseeville, R.; De Clerck, R.; De
ewes, H.W.; Mayer, K.F.X.; Scheller, C.
Submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15409
A:Accession: T01350
A:Molecule type: DNA
A:Residues: 1-392 <BEV>
A:Cross-references: UNIPROT:Q9SUU1; EMBL:AL034567
A:Experimental source: cultivar Columbia; BAC clone F8B4
C:Genetic:
A:Map position: 4
A:Intons: 181/3; 235/3
A:Note: F8B4.100

Query Match      47.0%; Score 1041; DB 2; Length 392;
Best Local Similarity 64.9%; Pred. No. 1.8e-71;
Matches 203; Conservative 47; Mismatches 59; Indels 4; Gaps 2;

Qy      92 EAGVQAKQAKKAKKQOLSLRKVVKIKNPHLRRLVSGAIAVARSRTFVAPLETIRTHM 151
Db      83 EEEVNVNKKRKKKKGGULT--KIKIANPSLRLLSGAVAGVSRVVAPLETIRTHM 139
Qy      152 VGSAGDMSAGVFWIRTEGMPGLFRGNVNVLRVAPSKAIEHTYDTAKYITPEAGE 211
Db      140 VG--SGNSSTVEFDIMKHBMGTGLFRGNLVNVIRVAPARAVELFVEETVKKLSPPHQ 198
Qy      212 PAKPIPTPLVAGLAGASTLCYPMELVTRLTITKDYDNLHAFVKIVRDEGPEL 271
Db      199 ESKPIPTPLVAGLAGASTLCYPMELVTRLTITKDYDNLHAFVKIVRDEGPEL 258
Qy      272 YRGAPSLIGVPPYAAANFYAETLRGVRRASKEEYGVNPTLLIGSAGAIASATFP 331
Db      259 YRGAPSLIGVPPYAAANFYAETLRGVRRASKEEYGVNPTLLIGSAGAIASATFP 318
Qy      332 LEVARKQMOVGANGROVKNVYHAMVCTLEKEGTGLVYRGVGPSCIKLMPAAGISPMCY 391
Db      319 LEVARKQMOVGANGROVKNVYHAMVCTLEKEGTGLVYRGVGPSCIKLMPAAGISPMCY 378
Qy      392 EACKIIVDEKED 404
Db      379 EACKIIVENNOE 391

RESULT 3
T01729
mitochondrial solute carrier protein homolog - Arabidopsis thaliana
N:Alternate names: protein A_IG002N01.16
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01729
R:Scheet, P.; Maggi, L.
Submitted to the EMBL Data Library, June 1997
A:Description: The sequence of A. thaliana IG002N01.
A:Reference number: Z14407
A:Accession: T01729
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A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-352 <SCH>
A:Cross-references: UNIPROT:O04619; EMBL:AF007269; NID:g2191126; PID:g2191150
A:Experimental source: cultivar Columbia
C:Genetic:
A:Map position: 4
A:Intons: 51/2; 67/3; 122/2; 135/1; 172/3; 210/3; 325/3
A:Note: A_IG002N01.16
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: mitochondrion

Query Match      20.9%; Score 462.5; DB 2; Length 352;
Best Local Similarity 33.8%; Pred. No. 1.4e-27;
Matches 120; Conservative 62; Mismatches 124; Indels 49; Gaps 12;

Qy      80 ADDVAAQLAAGAGAGVQKQAKK-AKQOLSLRKVVKIKNPHLRRLVSGAIAVARSRT 138
Db      3 SEDVKTESAAVSTYNLBEAREGVAPSYAKSI-----CKSLPAGVAGVSR 54
Qy      139 FVAPLETIRTHLMVGSAGDMSAGV--FWIRTEGMPGLFRGNVNVLRVAPSKAIEH 195
Db      55 AVAPLERMKILLQVQPHNIKSGTVQGLKHIRTGELGFLGNGNCAIRIVNSAVKF 114
Qy      196 FTYDTAKK----YLTPEAGEPAKVPDIPPLV--AGALAGVASTCTYPMELVTRITI 247
Db      115 FSYEQASNGILVYRORTGEMNAQL--TPLLRLAGAGATAGITAMGATYPMVWRRLTV 171
Qy      248 EKD----VYDNLHAAVVKVIRDEGPGLYRGLAPSLIGVPPYAAANFYAETLRG--VYR 301
Db      172 QTANSPYQYRGIMHAAVYRDEGPGLYRGLAPSLIGVPPYAAANFYAETLRG--VYR 231
Qy      302 RASG--KKEEVGNVPTLLIGSAGAIASATFPLEVARKQMOVGAVG-----GR 347
Db      232 NPYGLVNNELTYVTMLTGALIGTVGQTAYPLVDVIRRMQV--VGMKDAIAIVTGEGR 289
Qy      348 QV---YKQNVHAMVCTLEKEGTGLVYRGVGPSCIKLMPAAGISPMCEACCKIL 398
Db      290 STASLEYTGWVDAFRKTVRHEGFGALYKGLVPSNVKVPISALAFVYEMVKDVL 344

RESULT 4
T50686
peroxisomal Ca-dependent solute carrier [imported] - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: T50686
R:Weber, F.B.; Minestrini, G.; Dyer, J.H.; Weider, M.; Boffelli, D.; Compaszi, S.; Wehr
Proc. Natl. Acad. Sci. U.S.A. 94, 8509-8514, 1997
A>Title: Molecular cloning of a peroxisomal Ca2+-dependent member of the mitochondrial
A:Reference number: Z25180; NUID:97385133; PMID:9238007
A:Accession: T50686
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-475 <WEB>
A:Cross-references: UNIPROT:O18757; EMBL:AF004161; PIDN:AA69156.1
C:Keywords: peroxisome

Query Match      20.5%; Score 454; DB 2; Length 475;
Best Local Similarity 36.5%; Pred. No. 9.1e-27;
Matches 103; Conservative 63; Mismatches 102; Indels 14; Gaps 6;

Qy      124 RRLVSGAIAVARSRTFVAPLETIRTHLMVGSAGDMSAGVFWIRTEGMPGLFRGNVNV 183
Db      196 RQLAAGIAGAVRTSTAPDRKVMQVHGSSNMNIFGFRQMITEGGRSLMRNGNTN 255
Qy      184 VLNVAPSKAIEHTYDTAKKYLTPEAGEPAKVPDIPPLVAGALAGVASTCTYPMELVKT 243
Db      256 VIKIAPETAVKFWVVEGKKLLTEEG--QKIGFERFISGMAAGATAQTFFIYPMEMVKT 312
Qy      244 RLTIETK-DVYDNLHAAVVKVIRDEGPGLYRGLAPSLIGVPPYAAANFYAETLRGVYR 302
Db      313 RLAVGKTGYSGIYDCAKKILKIEGFGAFYKGVVNNLGIIPYAGIDLAVAYELKSHMD 372
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A:Residues: 1-418 <STO>
 A:Cross-references: UNIPROT:Q9C9R4; GB:AE005173; NID:96587866; PIDN:AAF18552.1; GSPDB:GN
 C:Genetics:
 A:Gene: T11111.12
 A:Map position: 1

Query Match 18.5%; Score 409.5; DB 2; Length 418;
 Best Local Similarity 29.1%; Pred. No. 1.9e-23;
 Matches 121; Conservative 69; Mismatches 159; Indels 67; Gaps 12;

39 SQSPESRSIDPFRRLPASVGLSLSHGAPVAREH-----DGKA 77
 12 SSSSTSSSIDLSNEAFSTGGLFLE--PPGVSSSFDSISSKCSDBELHFGYWRNKT 68
 78 RRAADVQHDLAAGEGVGKAKKAKKQQLSL-----KRVYKGNPHLR-----RL 126
 69 RLRSGNMFELSVLSKDRSEQQCKALQNDDEIPCKDNKRSVIGGVRRGTMTRKIL 128
 127 VSGALAGAVSRTPVAPLETIRTHLMVSGSADSMAGVFMIRTEGMPGLFRGNANVLR 186
 129 MAGAVAAVMSKTFIAPLERLKLLEYVRGQRNLV-VAASIAITQGLTFWKGNLNLVLR 187
 187 VAPSKAIEHFTYDTAKKYLTPPEGEPAKVPITPLVAGALAGVASTLCTYPMELVTRLT 246
 188 TAPFKAVNFCAYDTYRKQLKLAGNQEATNFER-FVAGAAAGITATVLCPLDITRTKL 246
 247 IE-KVYVDNLHAFVKIYVDEGPELYRGLAPSLIGVYAAANFAYETLAGVY----- 300
 247 ARGELGIGAFMYIQTGLFSLYKGLVPSISMSLGAVFYGVVDILKSSFLATPE 306
 301 -----RRASGKE-----EVGNVPTLLISAGALASTATPPLVARKOMQAVAG 346
 307 GKRRLDMKQGOELNALDRLLEIGPRTIMYGAHAGACREAVATPEVVRQLOM----- 361
 347 RQVYKVNVLHAM--CYLKEEGTAGLYRGLGPSCTKMPAGISFMCYACKKILV 399
 362 -QMGKKNKLNALMGFNIRGGIPALYAGLLPSLLQVLSASISYVVE-CMKIVL 415

RESULT 11

T22145
 hypothetical protein F43G9.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T22145
 R:Kerhavy, J.
 submitted to the EMBL Data Library, September 1996
 A:Reference number: Z19523
 A:Accession: T22145
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-294 <ML>
 A:Cross-references: UNIPROT:Q93717; EMBL:Z79755; PIDN:CAB02107.1; GSPDB:GN00019; CESP:F4
 A:Experimental source: clone F43G9
 C:Genetics:
 A:Gene: CESP:F43G9.3
 A:Map position: 1
 A:Introns: 7/3; 44/1; 106/2; 175/1; 201/3; 254/1
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 18.4%; Score 409; DB 2; Length 294;
 Best Local Similarity 34.3%; Pred. No. 1.3e-23;
 Matches 96; Conservative 65; Mismatches 101; Indels 18; Gaps 10;

126 LVSGAIGAVSRTPVAPLETIRTHLMVSGSADSMAGVFRW1---MRTEGMPGLFRGNANV 182
 18 LSAGAIAGALAKTTIAPLDRKTIYQVSSSTRGSPSAIKTKITLYRRENGFALYKNSA 77
 183 NVLRVAPSKAIEHFTYDTAKKYL-TPPEGEPAKVPITPLVAGALAGVASTLCTYPMELV 241
 78 TVARVVVPSQMFAPAEQYKLLKVDENG--SRTPVKR-YINGSLAATATATITVYPLDTR 134
 242 KTRLTEKOV-YDNLHAFVKIYVDEGPELYRGLAPSLIGVYAAANFAYETLRGVY 300

135 KARLSVSSKLYQSSLSKHFVTKYKEGQIQLYRGIVPTLIGVLPYAGSSFFYTELKIY 194
 301 RASGKEEVGNVPTLLISAGALASTATPPLVARKOMQAV-GRGVYKVNVLHAMVC 359
 195 RDHREBE-NSYYRNLFGMLAGLIGQSSSPYLDIVRRMQTRIDSGMPLRLIH---- 249
 360 ILEKEG-TAGLYRGKGPSCTKMPAGISFMCYACKKIL 398
 250 IYHTEGLKRGLYKSLSMWLKGPVAVGSFTTYE--KVL 286

RESULT 12

T04273
 hypothetical protein F20B18.290 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T04273
 R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohleisel, J.; Mewes, H.W.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z15263
 A:Accession: T04273
 A:Molecule type: DNA
 A:Residues: 1-325 <BEV>
 A:Cross-references: UNIPROT:Q9SZ19; EMBL:AL049483
 A:Experimental source: cultivar Columbia; BAC clone F20B18
 C:Genetics:
 A:Map position: 4
 A:Introns: 46/3; 144/3; 181/1; 242/3; 284/3
 A:Note: F20B18.290
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 18.2%; Score 403; DB 2; Length 325;

Best Local Similarity 31.1%; Pred. No. 4.2e-23;

Matches 97; Conservative 66; Mismatches 117; Indels 32; Gaps 9;

124 RLTVSAGIAGAVSRTPVAPLETIRTHLMVSGSAD-----SMAGVFRWIRTEGMPGLR 178
 19 KELINGGYTGIGAKTAVAPLERIK--ILFQRRBEPKRIAGVGSINKTKTEGLMGFPR 75
 179 GNAVNVLRVAPSKAIEHFTYDTAKKYLTPPEGEPAKVPITPLVAGALAGVASTLCTYPM 238
 76 GNGASVARIVFPAALHMYAYEYRRMIIFGPDTRTGLP-LDLVAGSPAGTAVLPTVPL 134
 239 ELVKTTRLT-----IEKVDYDNLHAFVKIYVDEGPELYRGLAPSLIGVYAAAN 289
 135 DLVRYTKLAVYQTCVKAIPVEQIIRGIVDCCFSYRRESGARGLRGVAPSLYGIFFYAGLK 194
 290 FYAVETLGVARRASGKEEVGNVPTLLISAGALASTATPPLVARKOMOV-----GAVG 345
 195 FYFYEEMK--RHVPEHKODISLKLVCSSVAGLQGLTLYPLDVVRKMOVRLYSANV- 250
 346 GRQVYKVNVLHAMCYLKEEGTAGLYRGLGPSCTKMPAGISFMCYACKKILVDEKED 404
 251 KEETRGIMQTLFKIARBEQWQQLFSGLSINVLTAVPSAIGFTYTDIMKHLRVPRE- 309
 405 GGAEPQESTET 416
 310 ----SPEAAVTV 317

RESULT 13

T48171
 hypothetical protein F7A7.20 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C:Accession: T48171
 R:Bevan, M.; Tetryn, N.; Ardiles, W.; Buyehaert, C.; Dasseville, R.; De Clerck, R.; De
 ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: Z24487
 A:Accession: T48171
 A:Status: preliminary

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 06:55:40 ; Search time 1054 Seconds
(without alignments)
158.887 Million cell updates/sec

Title: US-10-659-199-18

Perfect score: 2217

Sequence: 1 MAAAMAATTMTKNNRASLV.....TETGAGGQAPAKSSNGDRP 433

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1139.5	51.4	289	2	AAV31936 Wheat brl
2	1041	47.0	316	3	AAQ49412 Arabidops
3	1041	47.0	316	3	AAQ11516 Arabidops
4	1041	47.0	392	3	AAQ11515 Arabidops
5	1041	47.0	392	3	AAQ49411 Arabidops
6	1041	47.0	411	3	AAQ49410 Arabidops
7	1041	47.0	411	3	AAQ11514 Arabidops
8	757.5	34.2	379	6	AAQ38268 Rice grai
9	564.5	25.3	174	2	AAV31934 Soybean b
10	561.5	25.3	336	3	AAQ52582 Arabidops
11	561.5	25.3	336	3	AAQ14675 Arabidops
12	561.5	25.3	346	3	AAQ14674 Arabidops
13	561.5	25.3	346	3	AAQ52581 Arabidops
14	561.5	25.3	348	3	AAQ14673 Arabidops
15	561.5	25.3	348	3	AAQ52580 Arabidops
16	561.5	25.3	348	5	ABQ92372 Herbicida
17	462.5	20.9	352	3	AAQ30070 Arabidops
18	459	20.7	109	2	AAV31935 Wheat brl
19	457	20.6	477	4	AAQ79077 Human pro
20	457	20.6	477	5	ABQ11331 Human tra
21	457	20.6	477	7	ADQ09990 Human NOV
22	457	20.6	477	8	ADL15740 Novel hum
23	454	20.5	475	8	ADL15742 Rabbit pe
24	448	20.2	384	6	ADA54221 Human pro
25	448	20.2	468	5	AAE22927 Human tra

26	448	20.2	471	4	AAU27697
27	448	20.2	475	8	ADH42321
28	448	20.2	509	4	AAU27669
29	438	19.8	468	6	ABJ37928
30	438	19.8	468	7	ADK51034
31	438	19.8	468	8	ADH42319
32	437	19.7	326	8	ADG44080
33	425.5	19.2	469	3	AAV76084
34	425.5	19.2	469	4	AAV56023
35	425.5	19.2	469	5	ABQ72223
36	420.5	19.0	377	4	ABQ60506
37	420.5	19.0	508	4	ABQ22637
38	419.5	18.9	342	8	ADN20637
39	418.5	18.9	366	4	AAU40072
40	418.5	18.9	385	3	AAU42329
41	418.5	18.9	469	3	AAV66718
42	418.5	18.9	469	4	AAQ87554
43	418.5	18.9	469	4	AAQ65241
44	418.5	18.9	469	5	ABQ95879
45	418.5	18.9	469	6	ABU58056

ALIGNMENTS

RESULT 1	AAV31936
ID	AAV31936 standard, protein, 289 AA.
XX	XX
AC	AAV31936;
DT	21-DEC-1999 (first entry)
XX	XX
DE	Wheat brittle-1 partial polypeptide.
XX	XX
KW	Brittle-1; wheat; carbohydrate; starch; transgenic plant.
OS	Triticum aestivum.
XX	XX
PN	W09949047-A2.
PD	30-SEP-1999.
XX	XX
PF	22-MAR-1999; 99WO-US006583.
XX	XX
PR	26-MAR-1998; 98US-0079420P.
XX	XX
PA	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	XX
PI	Allen SM, Hitz WD, Lightner JB, Rafalaki JA;
DR	WPI; 1999-591098/50.
DR	N-PSDB; AA220025.
XX	XX
PT	Novel genes useful in studies of carbohydrate metabolism and function in plants.
XX	XX
PS	Claim 16; Page 42-43; 42pp; English.
XX	XX
CC	This sequence represents a portion of wheat brittle-1, a plastidic membrane transporter involved in the transport of ADP-glucose from the cytosol to the plastid where it is used for starch biosynthesis. The sequence was deduced from an isolated partial cDNA clone (see AA220025).
CC	The invention relates to isolated nucleic acid fragments (see AA220012-25) encoding plant carbohydrate biosynthetic enzymes (see AAV31923-36) selected from 1,3-beta-D-glucan synthase and brittle-1. It also relates to the construction of a chimeric gene encoding all or a portion of a carbohydrate biosynthetic enzyme, in sense or antisense orientation, where expression of the chimeric gene results in altered levels of carbohydrate biosynthetic enzyme in a transformed host cell. The availability of nucleic acids encoding these enzymes will facilitate studies of carbohydrate metabolism and function in plants, provide genetic tools for the manipulation of these pathways, and provide a means

CC to control starch and 1,3-beta-D-glucan biosynthesis in plant cells
XX Sequence 289 AA;
Query Match 51.4%; Score 1139.5; DB 2; Length 289;
Best Local Similarity 74.5%; Pred. No. 8.9e-102;
Matches 216; Conservative 37; Mismatches 36; Indels 1; Gaps 1;
QY 115 RKIGNPHLRVLGALAGAVSRTEVAPLEIRTHLMVSGSGADSMAGFPMIRTEGMP 174
DB 1 KIKGNHKLKRLIGSGIAGAVSKRTVAPLEIRTHLMVSGG-NSSTEVEDSIKNEGWT 59
QY 175 GLPFGNAVNLVAPSSAIEHFTYDTAKKYLTPPAGEPAKVPIDPPLVAGALAVASTLC 234
DB 60 GLPFGNLVNYVAPSSAIEHFTYDTAKKYLTPPAGEPAKVPIDPPLVAGALAVASTLC 119
QY 235 TYPELWVKTRLTITKQVYDNLHAFVKIVRDEGEGELVYRGALPELIGVPPAANFYAYE 294
DB 120 TYPELWVKTRLTITKQVYDNLHAFVKIVRDEGEGELVYRGALPELIGVPPAANFYAYD 179
QY 295 TLKGVRRASGKEEVGNVPTLLISAGAAIATATPFLPELVARKOMOVGAVGROVYKNVL 354
DB 180 TLKGVRRASGKEEVGNVPTLLISAGAAIATATPFLPELVARKOMOVGAVGROVYKNVL 239
QY 355 HAWYCILEKEGTAGLYRGLGPSCKIKMPAGISFMCYEACKKILVDEKED 404
DB 240 HALTLTLEDEGVGLYRGLGPSCKIKLVPAAGISFMCYEACKKILIEENE 289
RESULT 2
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ID AAG49412 standard; protein; 316 AA.
XX
AC AAG49412;
XX
XX 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62508.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
OS
XX Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
XX 06-SEP-2000.
XX
PD
XX
PF 25-FEB-2000; 2000EP-00301439.
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Best Local Similarity	64.9%;	Pred. No. 3.7e-92;		
Matches 203;	Conservative 47;	Mismatches 59;	Indels 4;	Gaps 2;

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 Db 7 EEELVNGEIRKKKKGGJTL--KIKANPSLRLLSGAVAGVSRTPVAPLETIRTHM 63

QY 152 VGSAGADNACVFRIMKRTGEGGLFRNAVNTLRVAASKAIEHTYDTAKKLTLPAGE 211
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Db 64 VG-SGGNSTEVSDDIMKEGWGLFRGLVNVIIRVARARAVELFVEETVNNKLSPHQ 122

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QY 332 LEVARKOMOVGANGROYKYNVLHAMYCLLEKSTAGLYRGSGPSCITLMPAGISFMCY 391
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RESULT 3

ID AAG11516 standard; protein; 316 AA.

AC AAG11516;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 10261.

KW Protein identification; signal transduction pathway; metabolic pathway;

KW termination sequence.

OS *Arabidopsis thaliana*.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

PR 25-FEB-1999

PR 09-MAR-1999

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PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
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PR 01-SEP-1999; 99US-0151930P.
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PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
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Query Match 47.0%; Score 1041; DB 3; Length 316;
Best Local Similarity 64.9%; Pred. No. 3.7e-92;
Matches 203; Conservative 47; Mismatches 59; Indels 4; Gaps 2;

QY 92 EAGVQAKAKAKAKKQOLSLRKVRKIGNPHLRSLVSGAAGASTPVPAPLETITHTM 151
DB 7 EEEVNVNGERKRRKKKGLTL---KIKIAPSLKRLLSGAVAGSKTVVAPLETITHTM 63
QY 152 VSSGADSVAGVFRWIMRTGEMGLFRGNAVNLVAPSKALIEHFTYDTAKKYLPEAGE 211
DB 64 VG-SGNSSTVEFSIDMKHEGWTGLFRGNLVNIVAPARAVALFVFETVKKLSPPHQ 122
QY 212 PAKVPPTPLVAGALAGVASTLCTYPMELVKTRLTIKQVYDNLHAPFKYVRDEPGL 271
DB 123 ESKIPPLASLAGACGVSQTLTLYPLELVKTRLTIQRGVYKGIQFAFKIRBEGPTL 182
QY 272 YRGLAPSLIGVPPYAAAFAYETLREGVYRRASGKEEVGNVPTLLGSAAGAIATATP 331
DB 183 YRGLAPSLIGVPPYAAAFAYETLREGVYRRASGKEEVGNVPTLLGSAAGAIATATP 242
QY 332 LEVARKQOVGAVGGRQVYKQVNLHANYCIIEKEGTAGLYRGLGPGSCIKLMPAAGISFMCY 391
DB 243 LEVARKQOVGAVGGRVYKQVNLHANYCIIEKEGTAGLYRGLGPGSCIKLMPAAGISFMCY 302
QY 392 EACKKILVDEKED 404
DB 303 EACKKILVDEKED 315

RESULT 4
AAG11515
ID AAG11515 standard; protein, 392 AA.

AC AAG11515;
XX
XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10260.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.

PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
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XX 19-APR-1999; 99US-0130077P.
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PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
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Query Match 47.0%; Score 1041; DB 3; Length 392;
Best Local Similarity 64.9%; Pred. No. 5; le-92;
Matches 203; Conservative 47; Mismatches 59; Indels 4; Gaps 2;

QY 92 EAGVQAKQAKKAKQOOLSRKVRKIGNPHLRRLVSGAIVAGVSRTPVAPLETIRTHLM 151
DB 83 EEEVVGGEKKRKKKKGLTL--KIKIANDPSLRRLISGAVAGVSRTPVAPLETIRTHLM 139
QY 152 VGSSGADSNAGVPRWIMRTIEGMPGLFRGNANVNLRAVPSKAIETHFTYDRAKKYLTPEAGE 211
DB 140 VG-SGNSSSTFEVSDIMKHEGWTGLFRGNLVNVIKVAFAVABLFFVEIVNKKLSPEHGQ 198
QY 212 PAKVPIPTPLVAGALGVASTLCTYPMELVKTRLTTEKDYVDNLHAFVKIVRDEGPGL 271
DB 199 ESKIPPIPASLAAACGVSQTLTLTPBELVKTIRLTIRGVYKQIPDAFLKIIIEBGPTEL 258
QY 272 YRGLAPSLIGVVEYAANFAVETLRGVYRRASGKEVEGNVPTLLIGSAGALASTATFP 331
DB 259 YRGLAPSLIGVVEYAANTVYAYDSLRKAYRSPFKOEKIGIETLTLGLSAGALSTATFP 318
QY 332 LEVARKOMQVGAAGVGRQVYNNVLIHMYCTIEKSGTGLIRGLGPSCTIKMPAGISPMCY 391
DB 319 LEVARKMQVGAAGVGRVYNNMLHALVTILIEHGIIGWYKGLGPSCLKIVPAAGISPMCY 378
QY 392 EACKKILVDEKED 404
DB 379 EACKKILLENNOE 391

RESULT 5
AAG49411
ID AAG49411 standard; protein; 392 AA.
XX AAG49411;
AC AAG49411;

XX 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 62507.
DE Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
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Query Match 47.0%; Score 1041; DB 3; Length 392;
Best Local Similarity 64.9%; Pred. No. 5,1e-92;
Matches 203; Conservative 47; Mismatches 59; Indels 4; Gaps 2;

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DB 83 EEEVNGEKRRKKGGLTL--KIKIANSRLRLSLGAVAGASRTVAPLEITIRHLM 139
QY 152 VGSAGADSMAGVFRKWMIRKSGMPLFRGNANVNLVAPSAKIEHFTDTAKYLTPEAGE 211
DB 140 VG-SGGSSTVEFSDIKHSGWIGLFRGNLVNVIKRAVAPAVELFVEITVKKLSPPHQ 198
QY 212 PAKVPIPTPLVAGALAVASTLCTYPMELVYKTRITIEKDYVDNLHAFAVKIVRDEGSEL 271
DB 199 ESKPIPIASLLAGACAGVSOTLLTYPLIELVYKTRITIQGVYKGFDAFLKIIREEGPTL 258
QY 272 YRGLAPBLIGVPPVPAANFAYETLRGVNRRASKEKEVGNVPTLLISAGALASTKTFP 331
DB 259 YRGLAPBLIGVPPVPAANFAYDLSLRKAYBSFSKQEKIGNIETLLISLAGALSTATFP 318
QY 332 LEVARKQMVGAVGGRQVYKNNVLHAMYCIIEKEGTAGLYRGLGPSCKLMPAAGISPMCY 391

DB 319 LEVARKQMVGAVGGRVYKNNVLHAMLVTLIEHGIIGWYKGLGPSCKLVPAGISPMCY 378
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DB 379 EACKTILENNOR 391

RESULT 6
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DT 18-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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Query Match 47.0%; Score 1041; DB 3; Length 411;

Best Local Similarity 64.9%; Pred. No. 5, 4e-92; Mismatches 59; Indels 4; Gaps 2;

Matches 203; Conservative 47;

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QY 332 LEVARKMOYGAVGGRGVYRNVLAHMYCILEKEGTAGLYRGLGPSCTKMPAAGISPMCY 391
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DT 17-OCT-2000 (first entry)
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KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
OS Arabidopsis thaliana.
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PR 29-OCT-1999; 99US-0162142P.

Query Match	47.0%	Score 1041,	DB 3;	Length 411;
Best Local Similarity	64.9%	Pred. No. 5.4e-92;		
Matches 203; Conservative	47;	Mismatches 59;	Indels 4;	Gaps 2;

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Db 159 VG-SGGSSTVEFSDIMKHGEHGTGLFRGLVNVIRVAPARAVELPVFETVAKKLSPEHQ 217

QY 212 PAKVPIPTPLVAGALAGVASTLCTYPMELVKTRLTIKDYDNLJHAFVKIVRDEGPGL 271

Db 218 ESKPIPASLLAGACAGVSQTLLTYPLEAVKTRLTIGRGVYKGIIDAFKRIREEGPEL 277

Db 278 YRGALPSLIGVPPAATNYFAVDSLRYKRYRSFSKOEKIGNIETLLIGSLAGALSTATP 337

332 LEVARKOMOVAVGGROVYKNTLHMYCTLEKEGTAGLYRGLGPGCIKLMPAGISFMCY 391

Db 338 LEVARKMQVAVSGRVYKNNLHALVTILEHEGILGWYKGLGSPCLKLVPAAGISPMCY 397

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AAE38268
ID AAE38268 standard; protein; 379 AA.

AA
AC
AAE38268;
VV

DT 20-NOV-2003 (first entry)
XX

Rise: abiotic stress tolerance; pathogen resistance; disease resistance;
KW XX
XX

grain quality; nutritional content; plant yield; BTI; plant.

XX
PN WC2003048319-A2.

AA
PD
YY
12-JUN-2003.

PF 27-NOV-2002; 2002WO-US038359.
XX

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Sainz MB, Salmeron J, Weislo L;
PI
vv

DR WPI, 2003-505288/47.
DR N-PSDB; AAD57636.

PT New nucleic acid from *Oryza sativa*, useful for altering abiotic stress tolerance

PT nutritional content or yield in a plant.
XX

XX The invention relates to nucleic acid molecules from rice encoding

CC proteins for abiotic stress tolerance, enhanced pathogen or disease
CC resistance and altered nutritional quality. The sequences of the

CC invention are useful for altering abiotic stress tolerance, pathogen or
 CC disease resistance or the grain quality, nutritional content or yield in
 CC a plant. The present sequence is rice grain quality and nutritional
 CC composition protein, Brl

XX
 SQ Sequence 379 AA;

Query Match 34.2%; Score 757.5; DB 6; Length 379;
 Best Local Similarity 57.4%; Pred. No. 1.7e-64;
 Matches 170; Conservative 32; Mismatches 65; Indels 29; Gaps 8;

QY 1 MAAMAATTMTYTKNNRNASLVNDK-NMLRPVPEVAPFMSQPE---SRSLD---FPRRA 53
 D 1 MAATMVA--MSAKSKNSVLTLEKKQGVSVPOLPELRFPMDLHEDKGSLSLHGSASPHCG 58
 QY 54 LFASVGLSLSHGAPVPA---REHDGKARPADDVAAHQAA-----GEAGYQK 97
 D 59 LFASVGLKVTAAAPAVAPSPAEHDFKLPFADHCIRYSSAVGYOVPGETEASVNEEVD 118
 QY 98 AQAQAKAKKQQLSLRYKVRKIGNPHLRSLVSGAIVASRTFVAPLETIRTHLMVSSGA 157
 D 119 GKAVKAKKRRGL---KLIKIKGNPHLRSLVSGAIVASRTFVAPLETIRTHLMVSSNG- 174
 QY 158 DSMAGVPRWMTKGMPEGLFRGNAVNVLRVAPSKAIEHFTYDIAKKYITPEAGSPAKVPI 217
 D 175 DSMTEVFQSIKMTGWTGLFRGNFNVLRVAPSKAIEHFTYDIAKKYITPEADESPKTPF 234
 QY 218 PTPVAGLAVGASTLCYPMELVKTIRLTIEKDYNDLHAFFKIVTDEGGELYR 273
 D 235 PPSLIGALAGVSSSLCTYPLELTKIRLTIEKDYNNELHAFVKILBEGFSALPR 290

RESULT 9

AA31934
 ID AA31934 standard; protein: 174 AA.

XX
 AC AA31934;

XX
 DT 21-DEC-1999 (first entry)

XX
 DE Soybean brittle-1 partial polypeptide.

XX
 KM Brittle-1; soybean; carbohydrate; starch; transgenic plant.

XX
 OS Glycine max.

XX
 FH Key Location/Qualifiers

FT Misc-difference 147 /note= "encoded by TAG"

FT Misc-difference 167 /note= "encoded by CNA"

FT Misc-difference 171 /note= "encoded by TAG"

FT Misc-difference 173 /note= "encoded by CAN"

XX
 PN WO9949047-A2.

XX
 PD 30-SEP-1999.

XX
 PF 22-MAR-1999; 99WO-US006583.

XX
 PR 26-MAR-1998; 98US-0079420P.

XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX
 PI Allen SM, Hiltz WD, Lightner JE, Rafalski JA;

XX
 DR WPI: 1999-591098/50.

XX
 DR N-PSDB; AA220023.

PT Novel genes useful in studies of carbohydrate metabolism and function in
 PT plants.

XX
 PS Claim 16; Page 40-41; 42pp; English.

XX
 CC This sequence represents a portion of soybean brittle-1, a plastidic
 CC membrane transporter involved in the transport of ADP-glucose from the
 CC cytosol to the plastid where it is used for starch biosynthesis. The
 CC sequence was deduced from an isolated partial cDNA clone (see AA220023).
 CC The invention relates to isolated nucleic acid fragments (see AA220012-
 CC 25) encoding plant carbohydrate biosynthetic enzymes (see AA31923-36)
 CC selected from 1,3-beta-D-glucan synthase and brittle-1. It also relates
 CC to the construction of a chimeric gene encoding all or a portion of a
 CC carbohydrate biosynthetic enzyme, in sense or antisense orientation,
 CC where expression of the chimeric gene results in altered levels of
 CC carbohydrate biosynthetic enzyme in a transformed host cell. The
 CC availability of nucleic acid encoding these enzymes will facilitate
 CC studies of carbohydrate metabolism and function in plants, provide
 CC genetic tools for the manipulation of these pathways, and provide a means
 CC to control starch and 1,3-beta-D-glucan biosynthesis in plant cells
 XX

SQ Sequence 174 AA;

Query Match 25.5%; Score 564.5; DB 2; Length 174;
 Best Local Similarity 66.3%; Pred. No. 3.2e-46;
 Matches 112; Conservative 21; Mismatches 35; Indels 1; Gaps 1;

QY 133 GAVSRTPVAPLETIRTHLMVSSGADSMAGVPRWMTKGMPEGLFRGNAVNVLRVAPSKA 192
 D 3 GAVSRTPVAPLETIRTHLMVSSGADSMAGVPRWMTKGMPEGLFRGNAVNVLRVAPSKA 61
 QY 193 IEHFTYDIAKKYITPEAGSPAKVPIPTPLVAGLAVASTLCYPMELVTRLTIEKDY 252
 D 62 IELFAYDVTAKQSLSPKRGEPPIPIPPSSVAGVSSSLCTYPLELTKIRLTIVRGYV 121
 QY 253 DNLHAFVKIVRDEGPEGLRGLAPSLIGVPAANFVAXETLRGYR 301
 D 122 KNLDAFVRIVQEGPELTYRGLAPSKMNCNPFYATNYFYDILRAATR 170

XX
 AC AAG52582;

XX
 DT 18-OCT-2000 (first entry)

XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 66859.

XX
 KM Protein identification; signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.

XX
 OS Arabidopsis thaliana.

XX
 PN EP1033405-A2.

XX
 PD 06-SEP-2000.

XX
 PF 25-FEB-2000; 2000EP-00301439.

XX
 PR 25-FEB-1999; 99US-0121825P.

XX
 PR 05-MAR-1999; 99US-0123180P.

XX
 PR 09-MAR-1999; 99US-0123548P.

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 PR 23-MAR-1999; 99US-0125788P.

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Query Match	25.3%;	Score 561.5;	DB 3;	Length 336;
Best Local Similarity	39.9%;	Pred. No. 1.6e-45;		
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OY	184 VLIVAPSKAIEHPFYDTAKKYLTP-----EAGEPAKVPPIP-----TPL-VAGAL 226		
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OY	227 AGVASTLCYTPMELVKTRLTLTEKDVYDNLHAFAVKIVRDEGPGELVYRGLABSLIGVVPYA 286		
DB	157 AGIASTLVCHPLFVLKORLFTVSPETVPSLSLAIPRIFRADGIRGFVYGLGPTLVGMPLYS 216		
OY	287 AANFYAETLKGTVRRASGKEEVGNVPTLLIGSAAAGIASATPTPFLVPAKQOMGVAGVG 346		
DB	217 TCYVFMDKMTSCSKSKNKKALRPEMLVIGALAGLASTISPLEVARRRRLWVAGLKG 276		
OY	347 RQVKNVYLHMYCCTLEKEBGTAGLYRGLGPGSCIKLMPAGISFMVCEACKITLV 399		
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DT	17-OCT-2000 (first entry)		
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DE	Arabidopsis thaliana protein fragment SRQ ID NO: 14627.		
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XX	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KX	termination sequence.		
XX			
OS	Arabidopsis thaliana.		
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PN	EP1033405-A2		

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XX 17-OCT-2000 (first entry)
XX
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
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Query Match 25.3%; Score 561.5; DB 3; Length 348;
Best local Similarity 39.9%; Pred. No. 1.7e-45;
Matches 117; Conservative 75; Mismatches 82; Indels 19; Gaps 5;

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QY 184 VLRAVAPKALIEHFVYDRAKYLTP-----EAGEPAKVPIP-----TPI-VAGAL 226
DB 109 MIRIIFQALIEGLGFENWKRAMTSAQYKLEIDAKIEIGPSPSPISMTSPVAVAGAS 168
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DB 169 AGIASTLVCHPLEVTLKORLTVSPPIYPSLSLAIPRIFRADGIRGFVAGLGPITVGMPLPYS 228
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
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XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
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Db 289 -ECPPNMAALAEVVKKEGVWGLYRGWGASCLKVMPSSGLTWVFYEAMKDILL 340

Search completed: May 25, 2005, 13:58:00
Job time : 1059 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 06:42:19 ; Search time 4092 Seconds
(without alignments)
2435.245 Million cell updates/sec

Title: US-10-659-199-17

Perfect score: 1625
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1625	100.0	1625	9	US-09-796-766-17
2	1625	100.0	1625	17	US-10-659-199-17
3	678	41.7	1715	18	US-10-437-963-47977
4	674	41.5	1588	17	US-10-425-114-8901
5	673.4	41.4	675	17	US-10-260-238-3967
6	672.8	41.4	1578	17	US-10-425-114-16127
7	672.8	41.4	1666	17	US-10-425-114-25407
8	672.6	41.4	1213	17	US-10-260-238-1023
9	549	33.8	698	17	US-10-260-238-2898
10	539.4	33.2	640	17	US-10-260-238-3968
11	511	31.4	661	17	US-10-260-238-3969

12	482.2	29.7	1951	18	US-10-437-963-44128	Sequence 44128, A
13	477.2	29.4	1516	17	US-10-425-114-30842	Sequence 30842, A
14	477.2	29.4	1722	17	US-10-425-114-27699	Sequence 27699, A
15	477.2	29.4	2090	18	US-10-425-115-13272	Sequence 13272, A
16	475.6	29.3	1817	17	US-10-425-114-793	Sequence 793, App
17	440.4	27.1	1056	17	US-10-260-238-3974	Sequence 3974, App
18	435	26.8	1816	18	US-10-437-963-19933	Sequence 19933, A
19	424.4	26.1	1988	17	US-10-425-114-28457	Sequence 28457, A
20	424.4	26.1	2166	18	US-10-425-115-60739	Sequence 60739, A
21	400.4	24.6	787	18	US-10-437-963-47978	Sequence 47978, A
22	400.2	24.6	1267	9	US-09-796-766-19	Sequence 19, Appl
23	400.2	24.6	1267	17	US-10-659-199-19	Sequence 19, Appl
24	397.6	24.5	1140	18	US-10-491-733-25	Sequence 25, Appl
25	392.6	24.2	449	9	US-09-796-766-15	Sequence 15, Appl
26	392.6	24.2	449	17	US-10-659-199-15	Sequence 15, Appl
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35	249.8	15.4	606	18	US-10-767-701-15885	Sequence 15885, A
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ALIGNMENTS

RESULT 1
US-09-796-766-17
; Sequence 17, Application US/09796766
; Patent No. US20010047523A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BB1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796, 766
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Trichium aestivum
US-09-796-766-17

Query Match 100.0%; Score 1625; DB 9; Length 1625;
Best local similarity 100.0%; Pred. No. 0;
Matches 1625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGCACGTGAGGAGTGAAGAACTCTAGCAGGCGACGTATCAGTTCTGCT 60

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DB 61 TGCTTCTCGAGATGGCGCGCAATGCGCGAGACGACATGATGTGATCCAAAGAACACCGC 120
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US-10-659-199-17
Sequence 17, Application US/10659199
Publication No. US20040038287A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lightner, Jonathan
APPLICANT: Rafaleki, Antoni
TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
FILE REFERENCE: B1157 US CIP
CURRENT APPLICATION NUMBER: US/10/659,199
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US/09/796,766
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/668884
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: PCT/US99/06583
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: 60/079420
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 1625
TYPE: DNA
ORGANISM: Trilicium aestivum
US-10-659-199-17

Query Match 100.0%; Score 1625; DB 17; Length 1625;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5

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US-10-260-238-3967
; Sequence 3967, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyuki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell

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; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; SEQ ID NO 3967
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Triticum aestivum
; US-10-260-238-3967

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Query Match 41.4%; Score 673.4; DB 17; Length 675;
Best Local Similarity 99.9%; Pred. No. 2,7e-173;
Matches 674; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 121 GCGCGCGCGCATGACGAGCAGCGCGCGCTTCCGCTGAGAGTGGCGCGAGAGAGATGCA 180
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Qy 1212 CATGCCGCGCGCGCGATGCTCTTCAATGTGTGTCAGAGGCGTGCAGAGAGTACTTGTGCA 1271
Db 301 CATGCCGCGCGCGCGATGCTCTTCAATGTGTGTCAGAGGCGTGCAGAGAGTACTTGTGCA 360
Qy 1272 CGAGAAAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1331
Db 361 CGAGAAAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Qy 1332 AGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1391
Db 421 AGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Qy 1392 GGTGACCGTCAAAATGAGAAAGAAATGCGTGAATTTTGAAGCTTAAGCTTAT 1451
Db 481 GGTGACCGTCAAAATGAGAAAGAAATGCGTGAATTTTGAAGCTTATAGCTTAT 540
Qy 1452 TGGATTGAATCTTAAGTGAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1511
Db 541 TGGATTGAATCTTAAGTGAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Qy 1512 AACATGCTCGTTTCAATGATGCGTGAATGTTTATGACACCTTCTGTATCAATTC 1571
Db 601 AACATGCTCGTTTCAATGATGCGTGAATGTTTATGACACCTTCTGTATCAATTC 660
Qy 1572 AATAAGAGAGAGTTC 1586
Db 661 AATAAGAGAGAGTTC 675

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RESULT 6

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US-10-425-114-16127

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; Sequence 16127, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 16127
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3061-107-H7_FLI
US-10-425-114-16127

Query Match      41.4%; Score 672.8; DB 17; Length 1578;
Best Local Similarity 84.4%; Pred. No. 5.4e-173;
Matches 771; Conservative 0; Mismatches 133; Indels 9; Gaps 1;
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Db 1175 GCGGAGGACAGATGTACAAAGACGTCTCCACGCTATCTATGATCTCTCAAGAGAGAGG 1234
Qy 1166 GCACCGCGGAGCTTCAACCGGCGGTGCGCCCGACGCTGATCAAGTCAATGCGCGCGCG 1225
Db 1235 GCGCGGCGGAGCTGTACCGAGGTCTCGCCCTAGCTGATCAAGCTTCATGCGCGCGCG 1294
Qy 1226 GCATCTCTTCATGTGTATGAGAGCGCTGCAAGAAATCTTGTGACAGAGAAAGAGCG 1285
Db 1295 GCATCGCTTCATGTGTATGAGAGCGCTGCAAGAAATCTTGTGACAGAGAGAGATG 1354
Qy 1286 GCGGCGCGCGCGA 1298
Db 1355 AGGAGGAGAGGA 1367

RESULT 7
US-10-425-114-25407
; Sequence 25407, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 25407
; LENGTH: 1666
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3898-016-E4_FLI
US-10-425-114-25407

Query Match      41.4%; Score 672.8; DB 17; Length 1666;
Best Local Similarity 84.4%; Pred. No. 5.6e-173;
Matches 771; Conservative 0; Mismatches 133; Indels 9; Gaps 1;
```


Db	817	GATTGGCTTCAACCTTGTGTGACCTTACCCCATGAGACTGATCAAGACCAAGGATCACATCG	876
Qy	815	AGAAAGACGTGTAGACAAACCTCTCTCAACGCGTTTGTCAAGATCTGGCGACAGAAAGGCC	874
Db	877	AGAAAGACGTATACGACAAACGTCGCGACACGCGTTGTGAAGATCTTACGCGACGAGGGCC	936
Qy	875	CGGGGAACTGTACCGCGGGGCTGTGGGCCGAGAGCTGTATGGCGTGGTGGCCCTTACGCGGGG	934
Db	937	CGTCGAACTGTACCGTGGGCTGTGACACCAAGCTGATGCGCGTGGTGGCTGTACGCGGCT	996
Qy	935	CCAACTTCTACGCTTACGACGACGCTGCGCGGGGTGTACCGCGCGCGTGGGG-----	987
Db	997	GTAACTTCTACGCTTACGACGACGCTGGAAGCGGCTTACCGTGGCGACCGGGCGGCTC	1056
Qy	988	--AAAGAGAGTGGGCAACGTCCCGACGCTGTGATCGGGTCCGCGGGGCGGCATAG	1045
Db	1057	CCGCGCGGAGAGTGGGGCCCCCGGTGGCGACGCTGTGATCGGGTCCGCGGGCGGCATCG	1116
Qy	1046	CCAGACCGGCGCACGTTCCCGCTGAGAGTGGGGCGGGAACAAATGAGAGTGGGGCCCGCTGG	1105
Db	1117	CCAGTCTGAGCCAGTGTCCCGCTGAGAGTGGGCCCGGAACAAATGAGAGTGGGGCCCGCTGG	1176
Qy	1106	CGGGAGGACAGGTGTACAAAGACGTGCTGACGCGCATGTACTGTGATCTTCGAGAAGAGG	1165
Db	1177	GGGGAGGACAGGTGTACCAAGACGTCTCTCAAGCTATCTACTGATCTTCAAGAAAGAGG	1236
Qy	1166	GCACTCGCGGCTTACCGCGGGGCTGGGCCCCCAAGTCATCAAGTCATGCGCGCGCG	1225
Db	1237	GCGCGGCGGCTTACCGAGGCTCGGCGCTTACGTCATCAAGTCATGCGCGCGCGCG	1296
Qy	1226	GCATCTCTTATGTGCTACGAGGCTGTCAAGAAATCTTGTGACGAGAAAGAGG	1285
Db	1297	GCATGCTTATGTGCTACGAGGCTGTCAAGAAATCTTGTGACGAGAGATG	1356
Qy	1286	GCGGCGCGCGCGA	1298
Db	1357	AGGAGGAGAGGA	1369

RESULT 8
 US-10-260-238-1023
 : Sequence 1023, Application US/10260238
 : Publication No. US20040016025A1
 : GENERAL INFORMATION:
 : APPLICANT: Budworth, Paul R.
 : APPLICANT: Moushamey, Todd G.
 : APPLICANT: Brigsen, Steven P.
 : APPLICANT: Cooper, Bret
 : APPLICANT: Glazebrook, Jane
 : APPLICANT: Goffe, Stephen A.
 : APPLICANT: Kategilti, Fumiya
 : APPLICANT: Krepes, Joel
 : APPLICANT: Provar, Nicholas
 : APPLICANT: Riche, Darrell
 : APPLICANT: Zhu, Tong
 : TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 : FILE REFERENCE: 60111-NP
 : CURRENT APPLICATION NUMBER: US/10/260,238
 : PRIOR FILING DATE: 2002-09-26
 : PRIOR APPLICATION NUMBER: US 60/325,448
 : PRIOR FILING DATE: 2001-09-26
 : PRIOR APPLICATION NUMBER: US 60/325,277
 : PRIOR FILING DATE: 2001-09-26
 : PRIOR APPLICATION NUMBER: US 60/370,620
 : PRIOR FILING DATE: 2002-04-04
 : NUMBER OF SEQ ID NOS: 6077
 : SEQ ID NO 1023
 : LENGTH: 1213
 : TYPE: DNA
 : ORGANISM: *Oryza sativa*
 : US-10-260-238-1023

Query Match	41.4%	Score 672.6	DB 17	Length 1213
Beet Local Similarity	82.3%	Pred. No.5.6e-173		
Matches 825	Conservative 0	Mismatches 164	Indels 14	Gaps 4
QY	291	TGACGGGAAAGCTCGGCCCCCGCGACGACGTCGCAACACAGCTCCAGCGC-----	341	
DB	155	TGCGGCGAAGGCGCGGACCACTGCGAGTCGCGCGGACGCTCCGCGCGCGAGGCCGA	214	
QY	342	GGGCGAGCGGGCGCTCCGAAAGGCCCGAAGGCGAAMAAAGCCAAAAGACAGACTGAG	401	
DB	215	GGAAGCGGCGGGGAAAGAAAGGCAAGGCAAGGAGAAAGTGAAGGGCGGCGGCTGTCTC	274	
QY	402	TCTGAGGAAGGTGAGGGTCAAGATCGGCAACCCGCACTGCGGGGCTGTGTCAAGCGGC	461	
DB	275	GCTGAGGAAGGTGAGGGTGAAGATCGGAAACCCGCACTTTCGCGGCTGTGTGAAGCGGCG	334	
QY	462	CATGCGCGGCGCGGTGTGAGGACTTTTCGTGAGGCGCACTGGAGAGATCAGAGCGACCT	521	
DB	335	CATGCGCGGCGCGGTGTGAGGACTTTTCGTGAGGCGCGTGGAGACATCCGACCCACTT	394	
QY	522	GATGATGGGAGCTCCGCGCGCGACTCCATGCGCGGGTTTTCCGTGATCATGCGAC	581	
DB	395	CATGATGGGAGCTCGCGCGCGCGACTCCATGCGCGGAGTCTTCGCTGTGATCATGCGAC	454	
QY	582	GGAAGGGGTGCGCGGCTCTTCGCGGCGCAACCGCTCAACGTCCTCGCGTGGCGCAAG	641	
DB	455	GGAAGGGGTGCGCGGCTCTTCGCGGCGCAACCGCTCAACGTCCTCGCGTGGCGCCAG	514	
QY	642	CAAGGCCATC--GAGCACTTCACTTATGACAACGCGGAAAGATACCTGACCCCGAGGCC	699	
DB	515	CAAGGCCATCAGAGCAATTCACCTACGACACGCGCAAGAAATCTCACCCCGAGAGAC	574	
QY	700	GGCAGCGCAGGCAAGTCCCATCCCAACGCGGCTGTGCGCGGAGCGCTGCGCGAGTG	759	
DB	575	GGCAGCGCTGCGCAAGATCCCATATCCGCTCCCTGTGTCGCGGCGCCTTCCGCGGTTC	634	
QY	760	GCGTCAACCCGTGSCACCTATCCATGAGGCTGTCAAGACCCGTCTTCAACATGGA--GA	817	
DB	635	GCTTCAACCTGTGACCTATCCCATGAGGCTGTCAAGACCCGCTTCAACATGAGGA	694	
QY	818	AGGACGTGTAGACAACTCTCTCAACGCGTTCGTCAAGATGTGTGCGGACGAAAGCCCGG	877	
DB	695	AGGACGTGTAGACAAAGTGTGTGACCGCTTCGTGAAGATGTGTGCGGAAAGCGGCGCG	754	
QY	878	GGGAGCTGTACCGGGGCTGGCGCGCGGACCTGATCGGAGTGTGTCGATACGCGGCGCA	937	
DB	755	GGGAGCTGTACCGGGGCTGGCGCGCGGACCTGATCGGAGTGTGTCGATACGCGGCGCA	814	
QY	938	ACTTCTACGCTTACGAGACGCTG--CGGCGGCTGTACCGCGCGCTCGGGGAAAGAGAG	996	
DB	815	ACTTCTACGCTTACGAGAGCTGCGCGCTGTGTACCGCGCGCGCGCGGCGGCGGAC	874	
QY	997	GTCGGGCAACGTCCCGACGCTGTGATGGGTTCGCGGCGGCGCGCATACCGACACGCGC	1056	
DB	875	GTCGGGCGGCGCGGAGGCTGTGATGGGTTCGCGGCGGCGCGCATACCGACACGCGC	934	
QY	1057	ACGTTCCCGCTGAGAGTGTGGCGGGAACGATGAGAGTGGCGCGCGTGGGGGGAAGAG	1116	
DB	935	ACCTTCCCGCTGAGAGTGTGGCGGGAACGATGAGAGTGGCGCGCGTGGGGGGAAGAG	994	
QY	1117	GTCGACAAAGACGTGTGTGACGCGCATGTACTCTCTCGAAGAGAGGACCGCGCGG	1176	
DB	995	GTCGACCGCAACGTGTGTGACGCGCATGTACTCTCTCGGCGGAGAGGCGCGCGGCG	1054	
QY	1177	CTTACCGCGGAGCTCGGCGCCCAAGTCATCAATGCCCCGCGCGCGCATCTCTTC	1236	
DB	1055	CTTACCGCGGAGCTCGGCGCCCAAGTCATCAATGCCCCGCGCGCGCATCTCTTC	1114	
QY	1237	ATGTGCTACGAGGCTGCAAGAAAGATCTCTTGTGACGAGAAAG	1279	
DB	1115	ATGTGCTACGAGGCTGCAAGAAAGTACTGTCTGCAAGAGAGG	1157	

Query Match	33.8%	Score 549;	DB 17;	Length 698;
Best Local Similarity	92.7%	Pred. No. 2.5e-139;		
Matches 600; Conservative	0;	Mismatches 40;	Indels 7;	Gaps 2;

QY 541 GACTCCATAGCGCGGGTTTTCCGGTGATCATACGAGAGGGGTGCGCGCTCTTC 60
 Db 536 GACTCCATAGCGCGGGTGTTCGGTGATCATACGAGAGGGGTGCGCGCTCTTC 593
 QY 604 CGCGGCATCGCGCTCAAGTCTCTCCGCGTCCGCGCCAGCAAGGCGCAT 650
 Db 594 CGCGGCATCGCGCTCAAGTCTCTCCGCGTCCGCGCCAGCAAGGCGCTCTTC 640

```

RESULT 10
US-10-260-238--3968
Sequence 3968, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Karagiri Funiyaki
APPLICANT: Krepis, Joel
APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 3968
LENGTH: 640
TYPE: DNA
ORGANISM: Triticum aestivum
US-10-260-238-3968

```

Query Match	33.2%;	Score 539.4;	DB 17;	Length 640;
Best Local Similarity	94.2%;	Pred. No. 1e-136;		
Matches 619; Conservative	0;	Mismatches 21;	Indels 17;	Gaps 5;

QY	942	TTAGCGCTCAGAGACGCTGCGCGCGGCGGTACCGCGCGCGCGTCCGCGGAAAGAGAGGTGG	1001
Db	1	CTAGCGCTCAGAGACGCTGCGCGCGGTGTAC-C-CGCGCGTCCGCGGAGAGAGGTGG	59
QY	1002	CACGCTCCCGACGCTGTGATCCGGGTCCGCGCGCGCGCCATAGCCAGCACGACCGT	1061
Db	60	CAGGTGCGACGCTGTGATC-GTCCGCGCGCGGCGCATAGCCAGCACCGCACGTT	118
QY	1062	CCCGCTGAGGTGGCGCGGAAGCAGATGACAGTGGCGCGGTGGCGGAGGCAAGTGT	1121
Db	119	CCCGTGGAGGTGGCGCGAAGCAGATGACAGTGGCGCGGTGGCGGAGGCAAGTGT	178
QY	1122	CAGAGAGTGTGCACGCTCATGTACTGATCTCTGAGAAAGAGGCAACCGCGCGGCTTA	1181
Db	179	CAGAGAGTCTCTGCACGCTCATGTACTGATCTTCAAGAACGAGGCAACCGCGGACTTA	238
QY	1182	CCGGGGGTGGGCCCCAGCTGCATCAAGCTCATGCGCGCGCCGCGCATCTCTTCATGTG	1241
Db	239	CCGGGGGTGGGCCCCAGCTGCATCAAGCTCATGCGCGCGCCGCGCATCTCTTCATGTG	298
QY	1242	CTACGAGCTTCGCAAGAGATTACTTGTTCGACGAGAAAGAAACGCGCGCGCCCGAGCC	1301
Db	299	CTACGAGCTTCGCAAGAGATTACTTGTTCGACGAAAGAAAG-----CGAGCC	346
QY	1302	CCAGAGGAGACGAGACCCGACAGGCAGAGAGACAGCGCGCGCCCAAGAGCTCGAAGG	1361
Db	347	CCAGAGGAGACGAGACCCGACAGGCAGAGAGACAGCGCGCGCCCAAGAGCTTCAGAGG	406

RESULT 14
 US-10-425-114-27699 Application US/10425114
 ; Sequence 27699, Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 27699
 ; LENGTH: 1722
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB4738-065-E6_FLI
 US-10-425-114-27699

Query Match 29.4%; Score 477.2; DB 17; Length 1722;
 Best Local Similarity 68.7%; Pred. No. 1.4e-119;
 Matches 672; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
 311 CCGACGACGTGCGACACCACTCGACCGCGGGCGAGGGCGGTCCAGAAAGCCGCA 370
 592 CTAGGACAGTGGGTGACAGCTTATTAACCTAGAGGCGGTGAGAGAGGTGTG 651
 371 AGCGCAAAAAGCCCAAAAGACAGAGTGTGAGAGGTGAGGGTTCAGATCGCA 430
 652 ATGCTAAGGCAAGAAAGGACGCAAGAAAGTGGGGTGCAGTGAATTAATTTGG 711
 431 ACCCGACCTCGCGCGGTGTGAGAGGCGCCATCGCGCGCGGTGTGAGAGCTTTG 490
 712 ACCCAATTTGAGAGAGGTGTGAGAGCTATTCAGGTGCTGTTCCAGAGCTTTG 771
 491 TGGCGCAGTGGAGAGATGAGACGACCTGATGTTGGGGAGCTCCGGCCGACCTCA 550
 772 TGGCAGCAGTGGAGAGATGAGACTGATGTTGGGGAGCAAGG--TGACTCCA 828
 551 TGGCGCGGGTTTCCGTTGATCATGCGAGCGAGGGGTGGCCGCTTCCGCGCA 610
 829 TGAAGAGGTGTTCCAGTCAATCATGAACCTGAGGGGTGAGCTGGCTTTCCGTGGA 888
 611 AGCGCTCAAGCTCTCCGCGGTGCGCCCAAGCAAGGCGCATGAGCACTTCACTTACG 670
 889 ATCTGTCAATGTATTCGAGTTGCGCCAAAGCAAAACAATGAGCTTTTGGTATGATA 948
 671 CGGCGAAGAGTACCTGACCCCGAGAGCGCGGAGCGAGCAAGTGTCCCATCCCAAGC 730
 949 CTGCGCAAGAAATCTTGACTCCAAAGCTGATGATGCTCCAAAGACTTTCATCTCCAT 1008
 731 CGCTCGCGCGAGAGCTGCGCGAGTGGCGTCAACCTGTGCACTTATCCAGAGAGC 790
 1009 CACTTATGCTGAGAGACTTGGAGAGTCAAGCTCAACCTGTGCAATATCTTTGGAGT 1068
 791 TGGTCAAGACCCGTCTCAACATGAGAGAGAGCTGTACGAACAACCTCTCCAGCGGTG 850
 1069 TGAATTAAGACAGATGAGAGTGAAGAAAGATGTCTATAACAACCTCTCCAGCTTTG 1128
 851 TCAAGATGAGCGCGAGAGCGCGGGAGAGTGAACCGCGGGCTGGGGCGAGAGCTGA 910
 1129 TCAAGATTTTACAGAGAAAGAGTCAATCAGAGCTCAACGTGTTGAGAACCAAGCTGA 1188
 911 TGGCGGTGAGCTGAGCGGCGGCGCACTTCAAGCTTACAGAGAGCTGCGCGGTGT 970

Db 1189 TAGAGTGTGTCATATGCGCGCACTAATTAATCAAGCTTATGACACCTTAAGAGCTCT 1248
 971 ACCGCGCGCGGTGCGGGAAGAGAGGTGGGCAACGTCCGAGCTGTATGCGGTCCG 1030
 1249 ATAGAAAGCTTCAAGAGAGAGATGACAAACATCGAATCTCTTAATGTTGAG 1308
 1031 CGGCGGCGCGCATATGACAGACAGGCAAGTTCCTCGGTGAGGTGGCGGAGAGATGC 1090
 1309 CGCTGTGCTCATCTCAGACACTGCAACTTCCCTTTGAGGTGGCCCGAGCAATGC 1368
 1091 AGGTGGCGCGGTGGCGGAGGAGAGGTGTACAAAGACGTGTGACAGCCATGACTGCA 1150
 1369 AGGTAGAGAGAGTGAAGAGAGGAGGAGGAGTCTACAAAGATGTTCCATGCGCTTACTGCA 1428
 1151 TCTCGAAGAGAGAGGACCGCGGCTCTACCGCGGCTGTGGCCCGCAGCTGATCAAGC 1210
 1429 TAATGAGAGAGAGAGGAGGTTGGCGCTGTACAAAGGAGGCTCGAGCCGAGCTGATCAAGT 1488
 1211 TCATGCCCGCGCGCGCATCTCTTCATGTGCTACAGAGGCTGTCAAGAGATTAATTGTCG 1270
 1489 TGAATGCTGAGAGAGGAGTCTGTTATGTCTGCTACAGAGGCTGTAAAGATCTGTGTCG 1548
 1271 ACGAGAAAGAGAGCGCG 1288
 1549 AAGACATGAGAGTGTG 1566

RESULT 15
 US-10-425-115-13272 Application US/10425115
 ; Sequence 13272, Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(5322)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 13272
 ; LENGTH: 2090
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_112098C.1
 US-10-425-115-13272

Query Match 29.4%; Score 477.2; DB 18; Length 2090;
 Best Local Similarity 68.7%; Pred. No. 1.5e-119;
 Matches 672; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
 311 CCGAGAGCTGCGACACCACTGCGACCGCGGGCGAGGCGGCGCTCCAGAAAGCCCA 370
 723 CTGAGGCAATTTGAGTACAGGTTATTAATGACATGAAGCGAGTCAAGAGAGGTGTG 782
 371 AGCGCAAAAAGCCCAAAAGACAGAGTGTGAGAGAGTGAAGGTCAAGATCGCA 430
 783 ATGCTAAGGCAAGAAAGAGAGGAGCGCAAGAAAGTGGGTGAGAGCTGAATAATTAATTTGG 842
 431 ACCCGACCTGCGCGGTGTGTCAGCGGCGCATGCGCGCGCGGTGTGAGAGACTTTG 490
 843 ACCCAATTTGAGAGGCTGTGTTAGTGAAGTATGCAAGGTGCTGTTTCAAGAGCTTTG 902
 491 TGGCGCACTGAGAGAGTCAAGAGAGCACTGATGTGGAGAGCTTCGCGCGCACTCA 550
 903 TGGCACTGAGAGAGAGTCAAGAGAGTCACTTATGATGTGGAGCAAGG--TGACTCCA 959
 551 TGGCGGGGTTTCCGTTGATCATGCGGAGCGAGGGGTGGCGGCTCTTCCGCGCA 610
 960 TGAAGAGGTGTTCCAGTCAATCAATGAACCTGAGGGGTGAGCTGGGCTTTTCCGTGGA 1019

QY 301 GCTGCGCCGCGCAGACGTCGACACCAAGCTCGCAAGCCGCGGCGAGCGGCGCTCGAG 360
Db 301 GCTGCGCCGCGCAGACGTCGACACCAAGCTCGCAAGCCGCGGCGAGCGGCGCTCGAG 360
QY 361 AAGGCCCAAGAAAGGAAAAAGGCAAAAGAGAGAGTCTGAGAAAGGTGAAGGTC 420
Db 361 AAGGCCCAAGAAAGGAAAAAGGCAAAAGAGAGAGTCTGAGAAAGGTGAAGGTC 420
QY 421 AAGATCGGCAACCCGCACTGCGGCGGCTGATCAGCGGCGCATCGCGGCGCTGCG 480
Db 421 AAGATCGGCAACCCGCACTGCGGCGGCTGATCAGCGGCGCATCGCGGCGCTGCG 480
QY 481 AAGATCGGCAACCCGCACTGCGGCGGCTGATCAGCGGCGCATCGCGGCGCTGCG 540
Db 481 AAGATCGGCAACCCGCACTGCGGCGGCTGATCAGCGGCGCATCGCGGCGCTGCG 540
QY 541 GCGCACTTCATGCGCGGCGGCTTTCGCGTGAATCATGCGGAGCGAGGGGCTGCGGCTC 600
Db 541 GCGCACTTCATGCGCGGCGGCTTTCGCGTGAATCATGCGGAGCGAGGGGCTGCGGCTC 600
QY 601 TTCCGCGGCAACCGCGTCAACGCTCTCGCGGCTCGCGCAAGCAAGGCGCATGAGCACTTC 660
Db 601 TTCCGCGGCAACCGCGTCAACGCTCTCGCGGCTCGCGCAAGCAAGGCGCATGAGCACTTC 660
QY 661 ACTTACGACACGCGGAAAGAAAGTACCTGACCCCGGAGCGCGGCGAGCCAGCCAGGTC 720
Db 661 ACTTACGACACGCGGAAAGAAAGTACCTGACCCCGGAGCGCGGCGAGCCAGCCAGGTC 720
QY 721 ATCCCAACGCGGCTGCTGCGCGGAGCGCTGCGCGGAGTGGGTGAACCTGTGCACTAT 780
Db 721 ATCCCAACGCGGCTGCTGCGCGGAGCGCTGCGCGGAGTGGGTGAACCTGTGCACTAT 780
QY 781 CCCATGAGAGCTGCTCAAGAACCCGCTCAACCTCAAGAGAGCGTGAACGCAACCTCTC 840
Db 781 CCCATGAGAGCTGCTCAAGAACCCGCTCAACCTCAAGAGAGCGTGAACGCAACCTCTC 840
QY 841 CACGCGTTCGTCAGAGATCTGCGCGAGAGGAGGCGGAGGAGTGAACCGCGGCTGCG 900
Db 841 CACGCGTTCGTCAGAGATCTGCGCGAGAGGAGGCGGAGGAGTGAACCGCGGCTGCG 900
QY 901 CCGAGCTGATCGGCGGCTGCTGCGGAGCGGCGGAGGAGTGAACCGCGGCTGCG 960
Db 901 CCGAGCTGATCGGCGGCTGCTGCGGAGCGGCGGAGGAGTGAACCGCGGCTGCG 960
QY 961 CCGGCGGCTGATCGGCGGCTGCTGCGGAGCGGCGGAGGAGTGAACCGCGGCTGCG 1020
Db 961 CCGGCGGCTGATCGGCGGCTGCTGCGGAGCGGCGGAGGAGTGAACCGCGGCTGCG 1020
QY 1021 ATCGGCTGCGGCGGCGGCGGAGTGAACCGGCGGAGGAGTGAACCGGCGGCTGCG 1080
Db 1021 ATCGGCTGCGGCGGCGGCGGAGTGAACCGGCGGAGGAGTGAACCGGCGGCTGCG 1080
QY 1081 AAGCAGATGCGAGTGGGCGGCGGAGGAGGAGGAGTGAACCGGCGGCTGCG 1140
Db 1081 AAGCAGATGCGAGTGGGCGGCGGAGGAGGAGGAGTGAACCGGCGGCTGCG 1140
QY 1141 AATGATGCGATCTCGAGAAAGAGGAGGAGGAGGAGGAGTGAACCGGCGGCTGCG 1200
Db 1141 AATGATGCGATCTCGAGAAAGAGGAGGAGGAGGAGGAGTGAACCGGCGGCTGCG 1200
QY 1201 TGCACTCAAGCTCATGCGGCGGCGGAGTCTCTTCACTGCTGAGAGGCTGAGAGAG 1260
Db 1201 TGCACTCAAGCTCATGCGGCGGCGGAGTCTCTTCACTGCTGAGAGGCTGAGAGAG 1260
QY 1261 ATACTTGTGACGAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
Db 1261 ATACTTGTGACGAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
QY 1321 GGAAGGCGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
Db 1321 GGAAGGCGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
QY 1381 TGAAGCATTTATGCGAGCGGTCAAAATCAAGAAAGAAATGCGGTGATTTTGAAGT 1440

Db 1381 TGAAGCATTTATGCGAGCGGTCAAAATCAAGAAAGAAATGCGGTGATTTTGAAGT 1440
QY 1441 GTAGAGCCTATTGCGATGTAATCTTAAGCTGGAAGTGGCGCTTGAAGTGAATTTGCT 1500
Db 1441 GTAGAGCCTATTGCGATGTAATCTTAAGCTGGAAGTGGCGCTTGAAGTGAATTTGCT 1500
QY 1501 TTTGTTCAAGGAAATGCTGCTGCTTCAATGTAATGCGTGAATGATTTATGCACTTTCT 1560
Db 1501 TTTGTTCAAGGAAATGCTGCTGCTTCAATGTAATGCGTGAATGATTTATGCACTTTCT 1560
QY 1561 GTATCAATTCATTAAGAAAGAGTCCATTTTGAACCTTCAAAAAA 1620
Db 1561 GTATCAATTCATTAAGAAAGAGTCCATTTTGAACCTTCAAAAAA 1620
QY 1621 AAAA 1625
Db 1621 AAAA 1625

RESULT 2
US-09-796-766-19
; Sequence 19, Application US/09796766
; Patent No. 660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafaleki, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BIL157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796, 766
; PRIOR APPLICATION NUMBER: 2001-03-01
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 1267
; TYPE: DNA
; ORGANISM: Trilicium aestivum
US-09-796-766-19

Query Match 24.6%; Score 400.2; DB 4; Length 1267;
Best Local Similarity 66.8%; Pred. No. 1.2e-77;
Matches 586; Conservative 0; Mismatches 288; Indels 3; Gaps 1;

QY 415 AAGGTCAAGATGCGCAACCGGCACTGCGGCGGCTGCTGAGCGGCGCATGCGCGGCGC 474
Db 2 AAGATTAAAGTTGGAATTCACCTCAAGAGGCTATCATGCGGAGGAGTTGCAAGAGCA 61
QY 475 GTGTGAGAGCTTTCGTGCGGCGCACTGAGAGAGATGAGAGCGACCTGATGTTGGAGAG 534
Db 62 GTGTGAGAGCAATTTGCGGCTTGTGAGAGAGATTAAGAGACATTTGATGTTGGCAGG 121
QY 535 TCCGCGCGCACTTCATGCGCGGAGGTTTTCGCTGATGATGCGAGCGAGGAGGAGGAG 594
Db 122 AATGGAAATTCATCTACGAGAGGTGTTGAC--TTCATCATGAAAGATGAAGATGAGCT 178
QY 595 GGCCTCTTCCGCGGCAACCGGCTCAAGCTGCTGCGGCGGCGCAAGAGGCGCATCGAG 654
Db 179 GGGTTGTTCGCGGCAATTTGTTAATGTCATTCGAGTGGCCCGGAGCAAAAGAAATCGAG 238
QY 655 CACTTCACTTACGACACGCGGAGAAAGTACTTGAACCCCGGAGGCGCGGAGGCCAGGCAAG 714
Db 239 CTTTTCCTTGTATACAGCTAAGAGAGTTCCTAACCCCAATCTGGGAGAAAGACAGAG 298
QY 715 GTCCCATCCCAACGCGCTGCTGCGCGGAGCGCTGCGGAGTGGCGTCAACCTGTGTC 774
Db 299 ATCCCAATCCCTCTTCACTAGTGGCAGAGGCTTTGTGTGTGAGTCACTGCTGTGT 358

QY 775 ACCTATCCATGAGCTCGTCAAGACCCCTCTCAACCATCGAAGAGCGTGTACGAAC 834
DB 359 ACATACCCCTCTGAGACCTAATTAAGACTCGATTAACCATAGAGAGGTGTATGATAC 418
QY 835 CTCTCTCAAGCGCTTCTGTCAGATCTGTCGCGACGAGAGCGCGGAGCTGTACCGCGG 894
DB 419 TTCTCTCATGCTATTTGTAATAATTTGTCCTGTAAGAAAGGCGCTGTGCTGTATAGAGG 478
QY 895 CTGGGCGCGAGCTGATCCGCGGTGTCCTGATAGCGCGCGGCAACTTCTACCGCTACGAG 954
DB 479 TTAAACCCCAAGTCTAAATCGAGTGTGTCATATGCAAGCAACAATTCGCGTATGAC 538
QY 955 ACCTCTCGCGGCGCTGTACCGCGCGCGCTCGAGGAAAGAGAGGTGAGCAACGTCGCGAG 1014
DB 539 ACCCTTAAGAAAGGTGTACAAAGAAATGTTCAAGACAAATTAATCGCAACGTTTCAAC 588
QY 1015 CTGCTGATCGGCTCGCGCGCGCGCGCATAGCCAGCAACGCTTCCGCTGAGAGTG 1074
DB 599 CTGCTCATTTGGCTGTGCTGTGAGAGCATCTCAAGACATGCTCAATTTCTCTGAGGT 658
QY 1075 GCGCGGAAGCATGATGAGGTGGCGCGCTGAGGCGGAGCGAGGTGTACAAAGCGTGTG 1134
DB 659 GCTCGAAGCATGATGAGGTGGCGCGCTGAGGCGGAGGTGTATACAAAGCATGCTT 718
QY 1135 CACGCGATGTACTGATCTCTCGAAGAGAGGAGCAGCGCGGCTTACCGCGGCTCGCG 1194
DB 719 CAGCTCTCTGACCAATTTCTCGAGAGCAAGAGGCTTGGGCGCTTACAGAGCATGGG 778
QY 1195 CCCAGCTGATCAAGCTCATGCCCCGCGCGCGCATCTCTTCAATGTCTACGAGCGCTG 1254
DB 779 CTAAGTTGATGAGAGCTGTGGCTGTGCTGTGGATTTGTTATGTGTACGAAGCTTGC 838
QY 1255 AAGAAGATCTTGTCAACGAGAAAGAGAGCGCGCG 1291
DB 839 AAGAAGATCTGATTGAGAGAGAGCAATGAGCG 875

RESULT 3
US-09-796-766-15

/ Sequence 15, Application US/09796766
/ Patent No. 6660850
/ GENERAL INFORMATION:
/ APPLICANT: Allen, Steve
/ APPLICANT: Ratajski, Antoni
/ TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
/ FILE REFERENCE: BB1157 US CIP
/ CURRENT APPLICATION NUMBER: US/09/796,766
/ PRIOR FILING DATE: 2001-03-01
/ PRIOR APPLICATION NUMBER: 09/668884
/ PRIOR FILING DATE: 2000-09-25
/ PRIOR APPLICATION NUMBER: PCT/US99/06583
/ PRIOR FILING DATE: 1999-03-22
/ PRIOR APPLICATION NUMBER: 60/079420
/ PRIOR FILING DATE: 1998-03-26
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 15
/ LENGTH: 449
/ TYPE: DNA
/ ORGANISM: Trilicium aestivum
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (6)
/ NAME/KEY: unsure
/ LOCATION: (268)
/ NAME/KEY: unsure
/ LOCATION: (383)
/ NAME/KEY: unsure
/ LOCATION: (449)
US-09-796-766-15

Query Match 24.2%; Score 392.6; DB 4; Length 449;
Best Local Similarity 96.4%; Pred. No. 4e-76;
Matches 432; Conservative 0; Mismatches 12; Indels 4; Gaps 3;
QY 1 GGCAGTAGAGGAGTAGAGACTGAAAGACTCTCTAGGCAAGGAGCATGATGTTCTGTCT 60
DB 1 GGCANTTAGAGGAGTAGAGACTGAAAGACTCTTAGGCAAGGAGCATGATGTTCTGTCT 60
QY 61 TGCTTCTGTG-AGATGCGCGCGGCAATGAGCCCGAGAGCAATGATGATCCAAAGAAACCG 119
DB 61 TGCTTCTGTGAGATGAGTGGCGGCAATGAGCCCGAGAGCAATGATGATCCAAAGAAACCG 120
QY 120 CGCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 179
DB 121 CGCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 180 CCCTTGAAGCTGAGAGCCGAGCTCAGAGAGCTTGAATTCACAGAGGAGCTTGTTCG 239
DB 181 CCCTTGAAGCTGAGAGCCGAGCTCAGAGAGCTTGAATTCACAGAGGAGCTTGTTCG 240
QY 240 CAGCTGAGAGCTGAGAGCTTCCAGAGGCGCGCGCGGTAGGCGCGAGCATGACGAGAA 299
DB 241 CAGCTGAGAGCTGAGAGCTTCCAGAGGCGCGCGCGGTAGGCGCGAGCATGACGAGAA 300
QY 300 GCGTGGCGCGCGAGAGAGTGTGACACC-AGCTGAGAGCGCGGCGAGGCGGCGTCC 358
DB 301 GCGTGGCGCGCGAGAGAGTGTGACACCAGAGTGTGACAGAGTGTGACAGAGGCGGCGTCC 360
QY 359 AGAAGGCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 416
DB 361 AGAAGGCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
QY 417 GGTCAAGATCGGCAACCGGACCTGCGG 444
DB 421 GGTCAAGATCGGCAACCGGACCTGCGG 448

RESULT 4

US-09-796-766-13

/ Sequence 13, Application US/09796766
/ Patent No. 6660850
/ GENERAL INFORMATION:
/ APPLICANT: Allen, Steve
/ APPLICANT: Ratajski, Antoni
/ TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
/ FILE REFERENCE: BB1157 US CIP
/ CURRENT APPLICATION NUMBER: US/09/796,766
/ PRIOR FILING DATE: 2001-03-01
/ PRIOR APPLICATION NUMBER: 09/668884
/ PRIOR FILING DATE: 2000-09-25
/ PRIOR APPLICATION NUMBER: PCT/US99/06583
/ PRIOR FILING DATE: 1999-03-22
/ PRIOR APPLICATION NUMBER: 60/079420
/ PRIOR FILING DATE: 1998-03-26
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 13
/ LENGTH: 1089
/ TYPE: DNA
/ ORGANISM: Glycine max
US-09-796-766-13

Query Match 18.6%; Score 303; DB 4; Length 1089;
Best Local Similarity 62.5%; Pred. No. 1.7e-56;
Matches 509; Conservative 0; Mismatches 300; Indels 6; Gaps 2;

QY 469 GCGCGCGCTGTCAGAGACTTTTCTGCGCGCACTGAGAGCATGAGAGCGACTGATGCTG 528
DB 7 GGTGCAGTGTCAAGAGACCGCTGCGCACCGTTGGAACCATTAAGACATCTATTGTATGGG 66
QY 529 GCGAGCTCGCGCGCGAGCTCCATGCGCGGCGGTTTCCGATGATCATGCGAGCGAGGCG 588

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Db      67 GGGAGCTGTGGGCAATGATCAATTCAGATGTTT---CAATCTATTATGAGACCGATGGA 123
Qy      589 TGGCCCGGCTCTTCCCGGCAACGCCGTCAACGCTCCGCGTCCGCGCAAGCAAGGCC 648
Db      124 TGGAAAGGCTTGTTCAGAGGCAATTTGTAAACATTCATCCAGTTGGCCCAAGCAAGCC 183
Qy      649 ATCGAGCACTTCACTTACGACACGCGCAAGAAAGTACTGACCCCGGAGGCGCGAGCCA 708
Db      184 ATTGAGTATTATGATATGACATGTCAAGAAAGCAATATATCTCCGAAACCTCGAGAGCAG 243
Qy      709 GCCAAGTTCCTCCATCCCAAGCCGCTGTGCGCGGAGAGCGCTGCGCGGAGTGGCTCAAC 768
Db      244 CCTTAAATCCCAATTTCCCTCTCATCAATTCGCGGTGTGTGTGTGTGTGTGTGTGTGT 303
Qy      769 CTGAGCACTTATCCATGAGAGCTGTCAAGACCCGCTCAACCATCGAAGAGAGTGTATC 828
Db      304 CTATGATCAATACCTCTTGAACCTACTCAAACTGCGCTCACTGTTCAAGAGGGGTGTAC 363
Qy      829 GACAACCTCTCCACAGCGGTTCTGTCAGATCTGCGCGCAAGAGGCGCGGAGAGCTGTAC 888
Db      364 AAGAATCTTACTCGAAGCATTTGTGAGATGCTTCAAGAGAGAGTCTCGAGATTTGTAT 423
Qy      889 CGCGGCTGCGCGCGCAAGCTGTATGCGGTGTGCTGACGCGCGCAACTTCTACGCC 948
Db      424 AGGGGCTCGCGCTAGCTAATGTGTATGCTTATGCTGCAAACTACTTTGCT 483
Qy      949 TAGAGAGCGTGGCGGGGTGTACCGCGCGGTGCGGAAAGAGAGGTGGCAAGTC 1008
Db      484 TATACACACTTAAAGAAAGCTTACAGAAAGAAAGCTTCAAAAGAGAGATTTGGAAATGTG 543
Qy      1009 CCGAGCTGTGATGCGGTGCGCGCGCGCGCAATAGCAGACAGGCAAGCTTCCGCTG 1068
Db      544 ATGACTCTTCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 603
Qy      1069 GAGGTGGCGGAGAGCAAGATGAGTGGGCGCGCTGGCGGAGAGCAAGTGTACAGAAC 1128
Db      604 GAGGTGGCTGCTAAGCATATGCAAGCTGGGCTCTAAATGGAAGACA---ATATGGGAAC 660
Qy      1129 GTGTGACGCGCATGTACTGTATGCTGAGAGAGAGGAGCGCGCGGCTCTACCGGGG 1188
Db      661 ATGCTTATGACATTTGTGAGATATCTTGAAGAAAGAGAGTGTGTGTGTGTGTGTGTGT 720
Qy      1189 CTCGCGCCCAAGCTCATCAAGCTCATGCGCGCGCGCATCTCTTCATGCTGCTACGAG 1248
Db      721 TTGGGACCAAGTCTTAAATTTGTTCTGCTGCTGCGGATTTCTTTCATGTGCTACGA 780
Qy      1249 GCCTGCAAGAAATCTTGTGACGAGAAAGAGA 1283
Db      781 GCTTGCAAGAGATCTTGTGAAGAAATGACAGAGA 815

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; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-796-766-3
Query Match      8.9%; Score 144; DB 4; Length 1062;
Best Local Similarity 55.3%; Freq. No. 6,7e-22;
Matches 301; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

Qy      737 TCGCCGAGAGGCTGCGCGGAGTGGCGCTCAACCTGTGCACTTATCCATGAGAGCTGTCA 796
Db      204 TTGCTGTGTGGCGCGCTGGAATGCTGGCACTATGATGTCATCTCTTGAAGTATTA 263
Qy      797 AGACCCGTCTCACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 856
Db      264 AGAGTGGCTGACCGTGGATTCAGATGACTTATCTTACATTAAGATTGCTTCAGAGAA 323
Qy      857 TCGTGGCGAGAGAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 916
Db      324 TATATGAACTGAAGATATCAGAGATCTTATTTCTGAGCTTGTCCCAACATTAATTGGA 383
Qy      917 TGTGTCGATACGCGGCGGCACTTCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 976
Db      384 TGTCTTCTTACAGACATGCTACTTATATGATGATGATGATGATGATGATGATGATGATG 443
Qy      977 GCGCGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1036
Db      444 GCCTACATTAAGAAAGAAATCTTGAAGCGTCTGAGCTAATATATAGAGAGCTGTACAG 503
Qy      1037 GCGCCATAGCAGACAGGCGCAAGTCTCCGCTGAGAGTGGCGGAGAGAGAGAGAGAG 1096
Db      504 GTCTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563
Qy      1097 GCGCGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1156
Db      564 GCGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 620
Qy      1157 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1216
Db      621 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 680
Qy      1217 CCGCGCGCGCATCTCTTCTATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1276
Db      681 CGAATTCGCGCATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 740
Qy      1277 AAGA 1280
Db      741 AAGA 744

RESULT 6
US-09-188-930-262
; Sequence 262, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Iorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Omrus, Rene
; APPLICANT: Muriison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 262
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Mouse
US-09-188-930-262
Query Match      6.2%; Score 101.2; DB 3; Length 1816;

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	Best Local Similarity	48.6%	Pred. No. 1,6e-12;	
	Matches	413;	Conservative	0; Mismatches 413; Indels 24; Gaps 4
QY	441	GGCGGGCTGTGTCAACGGCGCCATCGCCGGCCCGGTGTGAGAGACTTTGTGGCCCACT	500	
Db	622	GAGGCACTGGTGGCAGAGAGGTGGGAGGCGGCAAGTTTCAGAACCTGTGACGTGCCCTT	681	
QY	501	GGAGACGATCAGAGAGCCACTATGTGTGGGAGCTTCGGGCGCCAGC-----TCATGGC	554	
Db	682	GGACAGACTGAAGGTGGCTCATCAGGTCCATCCCTCCGCAACCAACATGTGATCGT	741	
QY	555	CGGGATTTTTCGGTGGATCATGTGGAGCCGAGGGGGTGGCCCGGCTTTCCGGGGCAACG	614	
Db	742	AGGTGGATTACACAGATGATTTCAGAAAGGGGAGCCAAATCATTCTGGCGGGGCAACGG	801	
QY	615	CGTCAACGTCCTCCCGGTTCGCCCAAGCAAGGCCATTCGAGCACTTCACTTACGACAGG	674	
Db	802	CATCATGTGCTCTCAAAATTTGCCCTGAGGTGGCCATCAAAATTCAATGAGCATAGACAGAT	861	
QY	675	GAAAGAGTACTTGACCCCGGAGCGCGGAGCCAGCCAAAGTCCCATTCGCCACCGCT	734	
Db	862	GAAACGG-----CTTGTGCGTAGTGATCAGAGAGACGTGAGGATTCAGAAAGGT	912	
QY	735	CGTCCCGGAGGCGTCCGCGGAGTGGCCGTCAACCTGTGACACTTATCCATGAGCTGT	794	
Db	913	TGTGGCAGGCTCTCTTGGCCGGAGCCATTGGCCAGATGAGCATCTCCAAATGAGGTTC	972	
QY	795	CAAGACCCGTCACCATTCAGAA---GGAAGTGAACGACACCTCTCCACGCTTGT	851	
Db	973	GAAAGCCCGAATGAGGCTTCGGGAAACAGGACAGTATCTCCGCAATGTGGAATTGGCAG	1033	
QY	852	CAAGATCTGTGGCGCAGAGAGCGCCGGGAGCTGTACCGGGGGTGTGGCGCGAGCTGAT	911	
Db	1033	GAGATCTTGGGTAAAGAGGTGTAGCTGCTTTCACAAAGCTACATCCCAACATCT	1092	
QY	912	CGCGGTGTGTCCTGACGGCGCGGCCAACTTCAACGCTTACGACGACGCTG-----CGCG	965	
Db	1093	GGGGATCATCCCTATGTGCTGGCATGACCTGACTGTCTATATGACATTTGAATAATCACTG	1154	
QY	966	CGTGTACCGCGCGCGCTCGGGGAAAGAGAGGTGGCAACGTCCGACGCTGTGATGG	1025	
Db	1153	GCTCCAGGCTTACGACAGTAAACATGTACAGACCCCGGTGTGTGTCGTGGCTGTGG	1212	
QY	1026	GTCCGGCGGGCGCCATACGCACGACGCGCACTTCCCGCTGAGAGTGGCGCGGACGA	1085	
Db	1213	TACTATCTTCCAGTATTTGTGTGCGACGCTGACGCTACCCACTACGACCTGTGTACGAGCCG	1272	
QY	1086	GATCAGAGTGGAGCGCGCTGTGGCGGAGGACAGGTATCAAGAACGATGTGACGACGATGA	1145	
Db	1273	GATCAGGACACAAAGCTCTCATTTGAGGGCGCACCTTAGAGTAACATAGACAGCTTTTCA	1333	
QY	1146	CTGCATCTCTGAGAAAGAGGACCCGCGGCTCTTACCGCGGCTCGGCGCCAGCTGAT	1205	
Db	1333	ACAGATTCTGGGAGACTGAGGGGGCTTTTGGGTCTACCGGGGGCTGGGCCCACTTCA	1392	
QY	1206	CAAGCTCATGCGCGCGCGCGGCTTCTTATGTGTCTACGAGGCTTGCAAGAGATACT	1265	
Db	1393	GAAAGTGTATCCCGGTGTGAGCATCAGTACGTGTCTACGAAACCTGAAGATCACT	1452	
QY	1266	TGTGAGAGG	1275	
Db	1453	GGGCGGTGAG	1462	

RESULT 7
US-09-312-283C-262
; Sequence 262, Application US/09312283C

```

/ APPLICANT: Munison, James G.
/ APPLICANT: Kumble, Krishanand D.
/ TITLE OF INVENTION: Compositions Isolated from Skin Cells
/ TITLE OF INVENTION: and Methods for their Use
/ FILE REFERENCE: 11000.1011c2
/ CURRENT APPLICATION NUMBER: US/09/312.283C
/ CURRENT FILING DATE: 1999-05-14
/ NUMBER OF SEQ ID NOS: 425
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 262
/ LENGTH: 1816
/ TYPE: DNA
/ ORGANISM: Mouse
US-09-312-283C-262

Query Match      6.2%; Score 101.2; DB 4; Length 1816;
Best Local Similarity 48.6%; Pred. No. 1.6e-12;
Matches 413; Conservative 0; Mismatches 413; Indels 24; Gaps 4;

QY 441 GCGGGGGTGTTCACGGCGGCCCATTCGCGGCGCGGTGTTCAGAGACTTTCGGGGCCACT 500
Db 622 GAGGACCTCTGTGTGCGAGGAGGTGGGGCGGGGAGTTTCCAGAACCTCGCACTGCGCCCT 681
QY 501 GGAAGCATCATGAGACGCATCATGTATGTGTGGAGACTCGCGGCGCGGAC-----TCCATGGC 554
Db 602 GGACAGATGTAAAGGTGTCTCATGCAAGTTCATGCTCTCCGCGAGCAACAATGTGATGT 741
QY 555 CGGGGTTTTCCGGTGTGATCATGCGGACGGAAGGGGTGGCCCGGCTCTTCCGCGGACGC 614
Db 742 AGGTGTATTACAACAGATGATTCGAGAAAGGGGAGCCAAATCATCTGTGGGGGCAACG 801
QY 615 CGTCAACCTCTCCGCGCTCGCGCCACGACAGGCCATGTGAGCATTTCACTTACGACACGC 674
Db 802 CATCATGTCTCTCAAAATTTGCCCTGTAGTCGGCCATCAATTCATGTGATGTAGCAT 861
QY 675 GAAGAAGTACTGACCCCGGAGGCGCGGAGCCAGCCAAAGGTCCCATCCCGACGGCGCT 734
Db 862 GAAACGG-----CTTGTGGTATGATCAAGAGCGGTGAGATTCACGAAAGCT 912
QY 735 CGTCGCCGAGAGCGCTCGCCGAGTGTGGCGTCAACCTGTGCACTTATCCATGTAGAGCTGT 794
Db 913 TGTGGCAAGGCTCTTGGCGCGGAGCATTTGCCCAAGTACATCTAACCAATGTAGGTTCT 972
QY 795 CAAGACCCGTCTACCATCGAAG--GACGTGTACGACCAACTCTCTCCACGCGTTCGT 851
Db 973 GAAAGCCCGAATGGCCCTCGCGAAACAGCACATGACTCGGCGATGTGCACTGTGCAG 1032
QY 852 CAATATCTGTGGCCACGAAGGCCCGGGGGAGCTGTACCGGGGCTGGCGCGCGAGCTGTAT 911
Db 1033 GAGATCTTGTGCTAAAGAGGGGTGTAGTGTGCTTTTCAAAAGGCTAATCTCCCAACATGCT 1092
QY 912 CGCGGTGGTGCCTTACGCGGCGCGGCAACTTTTACGCGCTTACGAGACGCTG-----CGCGG 965
Db 1093 GGGGATCATCTCCCTATGTGTGCTGAGCATGACCTATGTCTTATGAGACATTTGAAAAATACCTG 1152
QY 966 CGTGTACCGCGCGCGCTCGGGGAAAGAGAGTGGGCAACGTCCGACGCTGTGATCGG 1025
Db 1153 GCTCAAGGCTACCGCAGTAAACAATGTGACGACCCGGGTGTGTTCTGTCTCTGCGCTGTGG 1212
QY 1026 GTCCGCGCGCGGCGCCATAGCCACGACGCGCTCACTTCCGCTGGAAGTGTGGCGGAAAGCA 1085
Db 1213 TACTATCTCCAGTACTTGTGTGCGACGTGGCCAGCTACCTACTACCCCTGTGTCAAGAACCG 1272
QY 1086 GATCAGAGTGGGCGCGGTGGGCGGAGGAGAGGTGTACAAAGACGTGTGCAAGCATGTGTA 1145
Db 1273 GATGACAGGACACAGCTCTCATTTGAGGGCGACCTGAGAGTAACTATGAGACAGCTCTTCCA 1332
QY 1146 CTGCATCTCTGAGAAAGAGGCAACCGCGGCTTGTACCGCGGCTCGGCGCCAGCTGCAT 1205
Db 1333 ACAGATTTCTGGGAGCTAGAGGGGCGCTTTTGGGCTTTCACGGGGGCTGGCGCCCACTTCAT 1392
QY 1206 CAAGTCAATGCGCGCGCGGCGCATCTCTTCTATGTGTCTAGAGGCTTGCAGAAAGATCT 1265

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Db 1393 GAAGTGATCCCGCTGTGACATACGTAAGTGTCTACGAAAACTGTAAGATCACTT 1452
QY 1266 TGTGACGAG 1275
Db 1453 GGGCGTGCAG 1462

RESULT 8

US-09-270-767-1160
; Sequence 1160, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 1999-03-17
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1160
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1160

Query Match 5.8%; Score 94; DB 4; Length 986;
Best Local Similarity 49.8%; Pred. No. 5e-11;

Matches 303; Conservative 0; Mismatches 290; Indels 15; Gaps 2;

QY 673 GCGAAGAAGTACTGACCCCGAGCGCGGAGCCAGCCAGATCCCATCCCGACCG 732
Db 40 GAGCAGTGGCGTGCATCTGACATGTGACAAAGGACGACCAACAGAAAGTGTGCG 99
QY 733 CTGCTGCCGAGCGCTTCGCGGAGTGGCTCAACCTGTGACCTTATCCCATGAGCTC 792
Db 100 TTTTGGCTGGCTCCCTGCGGGAATCACCCTGACAGTGTGAGTATCTCTGAGCTG 159
QY 793 GTCAAGACCGCTCAACATC-----GAGAAGACGTGTACGACCACTCTCCAGCG 846
Db 160 GCACGCGCCGCGATGCGCGTACCGAATCGTATCTGCTATCGAGCGCTGCACAAATC 219
QY 847 TTGCTCAAGATCTGTCGCGACGAAAGCCCGGAGGCTGTACCGCGGCTGCGCGCGAGC 906
Db 220 TTGACCAAGATCTGGGTGAGAGAGGTCCGCGAGCGCTTCCGCGCTACGCGGACCC 279
QY 907 CTGATCGCGGTGTGTCGCGTACCGCGCGCACTTTACGCTTACGACGCTGCGCGGC 966
Db 280 GTTCTCGGCGTATCTCCCTATGCGGGAACCTCTTCTTCACTACGAGACTCTTAAGCG 339
QY 967 GTGTACCGCGCGGTGCGGGAAGAGAGGTGAGCAACGTCGAGCGCTGTATCGGG 1026
Db 340 GAATATCTATGATGTGTGCGGCAATTAACCCAAATCTTATGCTCACTGCGCTTGGT 399
QY 1027 TCCGCGCGCGCGCATAGCCAGCAGCCAGCTTCCCGCTGAGTGGCGCG----- 1079
Db 400 GCTGCGGCTGTGCGCGCGCAACCGCGCATATCATTTGGAATTGTGCGCGAAGA 459
QY 1080 --GAAGCATGTGAGTGGCGCGCGTGGGCGGAGCGAGTGTACAAAGATGCTGCAC 1137
Db 460 ATGACAGCAATGCGGCTGAAACAGCGCTGCGAGATCGTACCCCAACATCTTGAACAT 519
QY 1138 GCCATGTATGCAATCTCTGAGAGAGAGCGCCCGCGGCTTACCGGCGGCTTGGCCCC 1197
Db 520 CTGCTCAAGATCTATCTGTGAGAGAGCGGTCAAGAAAGGTTTCTACAAAGGACTTAAG 579
QY 1198 AGCTGATCAAGCTCATGCGCGCGCGCATCTCTTCAATGTGCTACGAGGCTGCAAG 1257
Db 580 AACTGATCAAGAGGAGCCATCGCGGTGGGCACTACAGCTTCTCAGCTACGATCTATCAG 639
QY 1258 AAGATACT 1265
Db 640 GCGTGGCT 647

RESULT 9

US-09-270-767-16442
; Sequence 16442, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 16442
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-16442

Query Match 5.8%; Score 94; DB 4; Length 986;
Best Local Similarity 49.8%; Pred. No. 5e-11;

Matches 303; Conservative 0; Mismatches 290; Indels 15; Gaps 2;

QY 673 GCGAAGAAGTACTGACCCCGAGCGCGGAGCCAGCCAGATCCCATCCCGACCG 732
Db 40 GAGCAGTGGCGTGCATCTGACATGTGACAAAGGACGACCAACAGAAAGTGTGCG 99
QY 733 CTGCTGCCGAGCGCTTCGCGGAGTGGCTCAACCTGTGACCTTATCCCATGAGCTC 792
Db 100 TTTTGGCTGGCTCCCTGCGGGAATCACCCTGACAGTGTGAGTATCTCTGAGCTG 159
QY 793 GTCAAGACCGCTCAACATC-----GAGAAGACGTGTACGACCACTCTCCAGCG 846
Db 160 GCACGCGCCGCGATGCGCGTACCGAATCGTATCTGCTATCGAGCGCTGCACAAATC 219
QY 847 TTGCTCAAGATCTGTCGCGACGAAAGCCCGGAGGCTGTACCGCGGCTGCGCGCGAGC 906
Db 220 TTGACCAAGATCTGGGTGAGAGAGGTCCGCGAGCGCTTCCGCGCTACGCGGACCC 279
QY 907 CTGATCGCGGTGTGTCGCGTACCGCGCGCACTTTACGCGCTTACGAGCGCTGCGCGGC 966
Db 280 GTTCTCGGCGTATCTCCCTATGCGGGAACCTCTTCTTCACTACGAGACTCTTAAGCG 339
QY 967 GTGTACCGCGCGGTGCGGGAAGAGAGGTGAGCAACGTCGCGAGCTGTATCGGG 1026
Db 340 GAATATCTATGATGTGTGCGGCAATTAACCCAAATCTTATGCTCACTGCGCTTGGT 399
QY 1027 TCCGCGCGCGCGCATAGCCAGCAGCCAGCTTCCCGCTGAGTGGCGCG----- 1079
Db 400 GCTGCGGCTGTGCGCGCGCAACCGCGCATATCATTTGGAATTGTGCGCGAAGA 459
QY 1080 --GAAGCATGTGAGTGGCGCGCGTGGGCGGAGCGAGTGTACAAAGATGCTGCAC 1137
Db 460 ATGACAGCAATGCGGCTGAAACAGCGCTGCGAGATCGTACCCCAACATCTTGAACAT 519
QY 1138 GCCATGTATGCAATCTCTGAGAGAGAGCGCGCGGCTTACCGGCGGCTTGGCCCC 1197
Db 520 CTGCTCAAGATCTATCTGTGAGAGAGCGGTCAAGAAAGGTTTCTACAAAGGACTTAAG 579
QY 1198 AGCTGATCAAGCTCATGCGCGCGCGCATCTCTTCAATGTGCTACGAGGCTGCAAG 1257
Db 580 AACTGATCAAGAGGAGCCATCGCGGTGGGCACTACAGCTTCTCAGCTACGATCTATCAG 639
QY 1258 AAGATACT 1265
Db 640 GCGTGGCT 647

RESULT 10

US-09-796-766-9
; Sequence 9, Application US/09796766
; Patent No. 660850
; GENERAL INFORMATION:

```

; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: B1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-796-766-9

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Query Match      5.5%; Score 89; DB 4; Length 1506;
Best Local Similarity 49.0%; Pred. No. 7e-10;
Matches 267; Conservative 0; Mismatches 275; Indels 3; Gaps 1;

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QY 735 CGTCCGCGGAGCGCTGCGCGAGTGGCTCAACCCCTGTGCACCTATCCCATGAGTGGT 794
DB 702 CATCCCGGTGACGCTGCTGGAATTCCTAGCACTCTTGATGACATCCCTTGAACTTTT 761
QY 795 CAAGACCCGCTCACCATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 854
DB 762 GAAAGACCGGTTAAGTGAAGTCTGAAACTTAACCTTAAGTGAAGTGAAGTGAAGTGAAG 821
QY 855 GATCGTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 914
DB 822 TATTTATATAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 881
QY 915 CGTGGGCGGCTGAGCGGCGGCGCAACTTCAAGCTTACGAGAGAGAGAGAGAGAGAGAGAG 974
DB 882 CATGCTTCATACAGTACATGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 941
QY 975 CCGCGCGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1034
DB 942 CCGAGACCAAAAGTAAAGAAATCTCTAAGCCGTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1001
QY 1035 GGGCGCCATAGCCAGACAGGCGCAAGTTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1094
DB 1002 AGGTTTACTGCAAGTACATTAAGTTCCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1061
QY 1095 GGGCGCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1154
DB 1062 GGGTGTCTTTCAGAGTAAAGTGGCCG--CCAAACATGGGAGAGAGAGAGAGAGAGAGAG 1118
QY 1155 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1214
DB 1119 TAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1178
QY 1215 GCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1274
DB 1179 GGCATCTCTGATATCACTGATGATGTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1238
QY 1275 GAAAG 1279
DB 1239 GAATG 1243

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RESULT 11
US-09-796-766-7
; Sequence 7, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan

```

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; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: B1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 1517
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-796-766-7

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Query Match      5.5%; Score 89; DB 4; Length 1517;
Best Local Similarity 49.0%; Pred. No. 7e-10;
Matches 267; Conservative 0; Mismatches 275; Indels 3; Gaps 1;

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QY 735 CGTCCGCGGAGCGCTGCGCGAGTGGCTCAACCCCTGTGCACCTATCCCATGAGTGGT 794
DB 697 CATCCCGGTGACGCTGCTGGAATTCCTAGCACTCTTGATGACATCCCTTGAACTTTT 756
QY 795 CAAGACCCGCTCACCATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 854
DB 757 GAAAGACCGGTTAAGTGAAGTCTGAAACTTAACCTTAAGTGAAGTGAAGTGAAGTGAAG 816
QY 855 GATCGTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 914
DB 817 TATTTATATAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 876
QY 915 CGTGGGCGGCTGAGCGGCGGCGCAACTTCAAGCTTACGAGAGAGAGAGAGAGAGAGAGAG 974
DB 877 CATGCTTCATACAGTACATGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 936
QY 975 CCGCGCGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1034
DB 937 CCGAGACCAAAAGTAAAGAAATCTCTAAGCCGTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 996
QY 1035 GGGCGCCATAGCCAGACAGGCGCAAGTTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1094
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QY 1095 GGGCGCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1154
DB 1062 GGGTGTCTTTCAGAGTAAAGTGGCCG--CCAAACATGGGAGAGAGAGAGAGAGAGAGAG 1118
QY 1155 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1214
DB 1114 TAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1173
QY 1215 GCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1274
DB 1179 GGCATCTCTGATATCACTGATGATGTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1233
QY 1275 GAAAG 1279
DB 1234 GAATG 1238

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RESULT 12
US-09-796-766-11
; Sequence 11, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS

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QY 1047 CACACGCGCCACGCTTCCCGTGAAGTGGCGCGAAGCAGATGAGTGGCGCCCGTGG 1106
 DB 885 CCGCGTGTCCACGCTGGCCACCGGGTTCCGGGAGAAAGTGTATCCGCATCTTTCAGACC 944
 QY 1107 CCGGAGGCGAGTGTACAGAACTGCTGCAAGCCATGTAATCTTCAGAAAGAGG 1166
 DB 945 GAGAGCGCTGTGTCAGAGACATCCGCCAGCTTCGAGCTTCAGACCGAAGAAAGAGCGCTT 1004
 QY 1167 CACGCGCGGCTTAACCGGCGGCTCGGCCAGCTGATCACTCATGCGCCCGCGCG 1226
 DB 1005 CGAGTCTGTGATTTGACAGCCACACGCGCTCATCTCTGTACAGGCGCCCAAGCGAG 1064
 QY 1227 CATCTCTTCATGTGTACAGAGCTTCGAGAAATATTGTGACAGAAAGAAAGAGCG 1286
 DB 1065 GAAAGAGAGAGAGCTCTACTCCGCTCAAGGCGCTGGCGGCGCCGACCTCAAGCTCAC 1124
 QY 1287 CCGCGCGCGGAGCGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1346
 DB 1125 CACCATCGAAGAGCCCATCGAAATGTTGTGGAGCGCTTCACAGGTGAGGTGAGCC 1184
 QY 1347 CAAG 1350
 DB 1185 CAAG 1188

RESULT 15

US-09-902-540-1193
 / Sequence 1193, Application US/09902540
 / Patient No. 6833447
 / GENERAL INFORMATION:
 / APPLICANT: Goldman, Barry S.
 / APPLICANT: Hinkle, Gregory J.
 / APPLICANT: Slater, Steven C.
 / APPLICANT: Wiegand, Roger C.
 / TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 / FILE REFERENCE: 38-10(15849)B
 / CURRENT APPLICATION NUMBER: US/09/902,540
 / PRIOR FILING DATE: 2001-07-10
 / PRIOR APPLICATION NUMBER: 60/217,883
 / NUMBER OF SEQ ID NOS: 16825
 / SEQ ID NO 1193
 / LENGTH: 21375
 / TYPE: DNA
 / ORGANISM: Myxococcus xanthus
 / FEATURE:
 / NAME/KEY: unsure
 / LOCATION: (1)..(21375)
 / OTHER INFORMATION: unsure at all n locations
 US-09-902-540-1193

Query Match 4.3%; Score 69.2; DB 4; Length 21375;
 Best Local Similarity 43.1%; Pred. No. 3.3e-05;

Matches 390; Conservative 0; Mismatches 508; Indels 6; Gaps 1;

QY 447 GCTGTCAAGCGGCGCATGCGCGCGCGCTGTGTGAGAGACTTGTGCGCCCACTGAGAC 506
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 QY 507 GATCAGAGACGACCTGATGATGAGGAGCTCCGCGCGCGACTCATGAGCGCGGTTTCCG 566
 DB 19827 GCGCACCCCGCAGGCGCGCTGTGTGTGCGGAGGCAACCTTTGACCGGGAACCTTT 19886
 QY 567 GTGATCATGCGAGAGAGAGGCTGCGCGCTTTTCGCGGCAAGCGCTCAACGTCTT 626
 DB 19887 CGAAAGCTTTCACCGGCTGACGCGGCTGCGCGGTGAGCCCGTCTCAGCGCGAAGCGGA 19946
 QY 627 CCGCGTGGCGCCAGAGAGAGGCTTGAAGACTTCACTTACAGACAGCGCGAAGAGTAAGT 686
 DB 19947 CATCTCAAGTCCATGAGGACATCTTAAGGAAAGAGCGTGGCGCGCGCGCGA 20006
 QY 687 GACCCGAGAGCGCGAGAGCGAAGGTCCTCATCCCGCGCTGTGTGCGCGAGC 746

DB 20007 CGACTTCAGGCGCGCGCGAGAGCCAGGTCGCAACTTGTGACAGCTGTCTGTGACG 20066
 QY 747 GCTGTGCGAGTGTGCTCAACCTGTGTGACCTATCCCATGAGACTGTCAAGACCGCTT 806
 DB 20067 CCGCACCCAGAGATTTGAGGCGTGTGAGACCGGCGCGGTGTGACGCGTGTGACTTACCTGTCT 20126
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 DB 20127 GCGCTACGCGTTTGACATTCGCGCTTCGAGACATTCATTGAACCGAGCGCACACAG 20186
 QY 867 CGAAGCGCGGAGAGCTGTACCGCGGCTGGCGCGAGCGCTGATCGGCGGTGTGCGGTA 926
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 QY 987 GAAAGAGAGGTGTGCGCAAGTCCCGAGCGCTGTGATCGGAGTCCGCGGCGCGCAATAGC 1046
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 QY 1047 CAGCAGGCGCAGCTTCCGCTGAGAGTGTGCGCGAGAGCAGATGCAAGTGTGCGCGCTGG 1106
 DB 20361 CCGCGTGTCAAGCTGTCCACCGCGCTTGGCGAGAGAGTGTATCCGATCTTTCAGACC 20420
 QY 1107 CCGGAGGCGAGTGTACAGAAAGTGTGTGACCGCATGTACTGTGATCTTCAGAAAGAGG 1166
 DB 20421 GAGAGCGTGTGTGACAGACATGCGCCAGCTTCGAGCCGAGAGAGAGCGCTT 20480
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 QY 1347 CAAG 1350
 DB 20661 CAAG 20664

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 06:24:34 ; Search time 8067 Seconds
(without alignments)
7667.588 Million cell updates/sec

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Perfect score: 1625

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Searched: 34239544 seqs, 19032134700 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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1: gb_est1:*
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7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	680.8	41.9	722	5	BQ807247 WHE358_E
3	663.6	40.8	856	5	AM448477 BRY_866 B
4	663.6	40.8	856	5	BQ609855 BRY_866 W
5	645	39.7	655	5	BQ606434 BRY_2295
6	640.6	39.4	710	7	CV054670 BNE11234
7	639.6	39.4	787	2	AM448382 BRY_646 B
8	639.6	39.4	787	2	BQ609766 BRY_646 W
9	594.4	36.6	686	5	BQ608893 BRY_4808
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11	592.4	36.4	700	1	AL507153 AL507153
12	577.8	35.6	700	1	AL506597 AL506597
13	573.6	35.3	897	6	CD433626 EL01N0313
14	559.2	34.4	784	2	BE413774 SCU002.H0
15	555.6	34.2	739	7	CK125192 BES182410
16	552	34.0	611	1	AL814614 AL814614
17	550.6	33.9	591	5	BQ241079 TAB05009D
18	549	33.8	550	5	BQ606767 BRY_2638
19	548.2	33.7	737	7	CK122138 BES182410
20	546.8	33.6	589	5	BQ609479 BRY_5410
21	540	33.2	765	6	CD434709 EL01N0327
22	538.8	33.2	559	4	BU235011 BU235011
23	535.6	33.0	577	5	BQ240466 TAB05017A
24	535.6	33.0	578	5	BQ606681 BRY_2549

25	532.6	32.8	588	5	BQ804590
26	532.4	32.8	592	1	AL810557
27	529.2	32.6	623	7	CV055671 WHE125B8
28	528	32.5	669	2	BE414349 SCU008.GO
29	526.2	32.4	576	5	BQ239046 TAB05037H
30	522.2	32.1	607	5	BQ238019 TAB05009D
31	522	32.1	539	2	BQ608979 BRY_4897
32	520	32.0	574	2	BE402432 CSB007H06
33	520	32.0	574	5	BQ607768 BRY_3663
34	512.4	31.5	524	2	AM448856 BRY_1667
35	512.4	31.5	524	5	BQ606051 BRY_1667
36	510.8	31.4	751	6	CD438567 EL01N0514
37	509.2	31.3	539	2	BE402546 CSB009A12
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39	506	31.1	639	5	BQ606449 BRY_2311
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41	502.8	30.9	548	1	AL812274 AL812274
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43	492.4	30.3	754	6	CD448019 EL01N0203
44	488.2	30.0	517	5	BQ606900 BRY_2776
45	482	29.7	482	2	BE402735 CSB011A09

ALIGNMENTS

RESULT 1
CD885431 724 bp mRNA linear EST 14-JUL-2003
LOCUS G118.001H02F010306 G118 Triticum aestivum cDNA clone G118001H02,
DEFINITION mRNA sequence.

ACCESSION CD885431
VERSION CD885431.1 GI:32650608
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE
AUTHORS Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
JOURNAL Poideae; Triticaceae; Triticum.
COMMENT 1 (bases 1 to 724)

REFERENCE
AUTHORS Genoplatte.
TITLE Genoplatte, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplatte

Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>
and <http://genoplatte-info.infobio.gen.fr>).

FEATURES

source
1..724
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/cultiar="rectal"
/db_xref="taxon:4565"
/clone="G118001H02"
/tissue_type="grain (118 degrees per day after
pollination)"
/clone_lib="G118"

ORIGIN

Query Match 42.4%; Score 689.4; DB 6; Length 724;
Best Local Similarity 97.0%; Pred. No. 9e-144;
Matches 702; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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DB 1 GTGAAGACTGAAGACTCTTGAAGGACGATGCTTGTCTTCTCTCGAGA 60
QY 74 TGGCGCGGCAATGCGCGGACGACCAATGCGGACCAAGCAACGCGCTGCTGCA 133

Db 61 TGGCGCGGCAATGCGGCAACGACATGATGACCAAGAACACCGCGCTGCTGCCA 120

QY 134 TGGACAAGAGAACTGGTTATTGCGGCGGCTCCCTGAGGTGCGCTTCTTGAGCTCGC 193

Db 121 TGGACAAGAGAACTGGTTATTGCGGCGGCTCCCTGAGGTGCGCTTCTTGAGCTCGC 180

QY 194 AGCCCAAGTTCAGAGAGTTCGATCTCCCAAGCAGGGGTCTGTTCCGACAGGTGGAGCTCA 253

Db 181 AGCCCAAGTTCAGAGAGTTCGATCTCCCAAGCAGGGGTCTGTTCCGACAGGTGGAGCTCA 240

QY 254 GCTGTGCTCCAGCGGCGCGCGCGGTAGCGCGCAGCATGACGGAGAAAGCTCGGCGCGCG 313

Db 241 GCTGTGCTCCAGCGGCGCGCGCGGTAGCGCGCAGCATGACGGAGAAAGCTCGGCGCGCG 300

QY 314 AGCAGCTGCGACACAGCTGCGACGCGCGGCGAGCGGCGGTTCAGAGAGCCGACAGG 373

Db 301 AGCAGCTGCGACACAGCTGCGACGCGCGGCGAGCGGCGGTTCAGAGAGCCGACAGG 360

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Db 361 GAAAAAGGCGAAAAAGCAGCAGCTGATGATGAGAGAGTGAAGGTCAAGATGCGCAAC 420

QY 434 CGACCTGCGGCGGCTGTCAGCGCGCGCATGCGCGCGCGCTGTCAGAGACTTTCGTG 493

Db 421 CGACCTGCGGCGGCTGTCAGCGCGCGCATGCGCGCGCGCTGTCAGAGACTTTCGTG 480

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QY 554 CGGCGGCTTTTCGCGGTGATCATGCGACAGAGAGGTGGCCCGGCTTTCGCGCGCAAG 613

Db 541 CGGCGGCTTTTCGCGGTGATCATGCGACAGAGAGGTGGCCCGGCTTTCGCGCGCAAG 600

QY 614 CGGCAAGCTCTCGCGGTGCGCGCAAGAGAGGCTTCAGAGACTTTCAGACAGG 673

Db 601 CGGCAAGCTCTCGCGGTGCGCGCAAGAGAGGCTTCAGAGACTTTCAGACAGG 660

QY 674 CGAAGAGTACCTGACCCCGGAGCGCGGAGGCGAGCCAGGCTCCATCCCAACGCGCGC 733

Db 661 CGAAGAGTACCTGACCCCGGAGCGCGGAGGCGAGCCAGGCTCCATCCCAACGCGCGC 720

QY 734 TCGT 737

Db 721 TCGT 724

RESULT 2

BO807247 722 bp mRNA linear EST 31-JUL-2002

LOCUS WH83588 BO8.11625 wheat developing grains cDNA library Triticum

DEFINITION aestivum cDNA clone WH83588_BO8.116, mRNA sequence.

ACCESSION BO807247

VERSION BO807247.1 GI:22031456

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 722)

Autenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin, K., Crossman, C., Fenton, R.D., Iazo, G.R., Pham, J., Rausch, C.J., Wilson, C., and Woo, J.

RAUSCH, C.J., WILSON, C., AND WOO, J.

THE STRUCTURE AND FUNCTION OF THE EXPRESSED PORTION OF THE WHEAT GENOMES - DEVELOPING GRAINS cDNA LIBRARY

Unpublished (2002)

Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

FEATURES

source

1..722

/organism="Triticum aestivum"

/mol_type="mRNA"

/cuiovar="Bute 86"

/db_xref="taxon:4565"

/clone="WH83588_BO8.116"

/issue_type="whole grains"

/dev_stage="3-44 days post anthesis seed"

/lab_host="E. coli SOLR"

/clone_lib="wheat developing grains cDNA library"

/note="Vector: Lambda ZAP II, excised phagemid; Site 1: EcoRI; Plants were grown under six following different environmental regimes in greenhouse, Environment 1) 240C/170C day/night, well-watered, with post-anthesis fertilizer, Environment 2) 240C/170C day/night, well-watered, without post-anthesis fertilizer, Environment 3) 370C/170C day/night, well-watered, with post-anthesis fertilizer, Environment 4) 370C/170C day/night, well-watered, without post-anthesis fertilizer, Environment 5) 370C/170C day/night plus drought, with post-anthesis fertilizer, Environment 6) 370C/170C day/night plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S. Autenbach and K. Cronin at USDA-ARS, Albany, CA. A cDNA library was made using poly (A) RNA, and the cDNA clones were in vivo excised to give pBlueScript SK(-) phagemids in the T7 Close lab (Chin, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (others)."

ORIGIN

Query Match 41.9%; Score 680.8; DB 5; Length 722;

Best Local Similarity 97.6%; Pred. No. 7.6e-142;

Matches 691; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 41 GGCAGTATCAGTCTGCTTCTGCTCTCGAGATGCGCGGAGATGCGCGGAGCA 100

Db 15 GGCAGTATCAGTCTGCTTCTGCTCTCGAGATGCGCGGAGATGCGCGGAGCA 74

QY 101 TGGTACCAAGAACACCGCGCTCGCTGCTCATGACAGAGAACTGGTTATGGGCG 160

Db 75 TGGTACCAAGAACACCGCGCTCGCTGCTCATGACAGAGAACTGGTTATGGGCG 134

QY 161 CGGTCCCTGAGGTGCTTCCCTTGGAGCTTCGACGCCCGGAGTCCAGAGGCTTGC 220

Db 135 CGGTCCCTGAGGTGCTTCCCTTGGAGCTTCGACGCCCGGAGTCCAGAGGCTTGC 194

QY 221 CAGCAGAGGCTGTTGCGCAGCGTGGAGTCTGAGCTGTCACAGCGCGCGCGGTAG 280

Db 195 CAGCAGAGGCTGTTGCGCAGCGTGGAGTCTGAGCTGTCACAGCGCGCGCGGTAG 254

QY 281 CGCGCAGCATGACGGAGAGGCTTGCGCGCGCGAGCATGTCGACACAGCTCCAGCG 340

Db 255 CGCGCAGCATGACGGAGAGGCTTGCGCGCGCGAGCATGTCGACACAGCTCCAGCG 314

QY 341 CGGCGAGGCGGCGGTCCAGAGGCGCGAGAGGCGAGAGGCGAGAGGCGAGCGTGA 400

Db 315 CGGCGAGGCGGCGGTCCAGAGGCGCGAGAGGCGAGAGGCGAGAGGCGAGCGTGA 374

REFERENCE	1 (bases 1 to 866)
AUTHORS	Clarke, B., Lambrecht, M. and Rhee, S. Y.
TITLE	Arabidopsis genomic information for interpreting wheat EST sequences
JOURNAL	Punct. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE	22478026
PMID	12590341
COMMENT	Contact: Lambrecht M The Arabidopsis Information Resource

Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rheeo@coma.stanford.edu.

FEATURES
Source Location/Qualifiers

1..856
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wynua"
/db_xref="taxon:4565"
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(days post anthesis)"
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Query Match 40.8%; Score 663.6; DB 5; Length 856;
Best Local Similarity 92.6%; Pred. No. 5.5e-138;
Matches 786; Conservative 0; Mismatches 50; Indels 13; Gaps 8;

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QY 14 GTGAAGAGCTGAAGAACTCTTAGGCGAGGCGACGTAATCATGTTCTGTCTTCTTCTCGAGA 73
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QY 74 TGGGCGGCGGCAATGCGCGCGGCGACGACAAATGTGACCAAGAAACACCGGCGCTCGCTGCA 133
Db 56 TGGGCGGCGGCAATGCGCGCGGCGACGACAAATGTGACCAAGAAACACCGGCGCTCGCTGCA 115
QY 134 TGACCAAGAAAGAACTGTTATTTGGCGCGGTCCTCGAGTGCCTTCCCTTGTGAGCTGCG 193
Db 116 TGGACAAAGAAAGAACTGTTCTTGGCGCGGTCCTCGAGTGCCTTCCCTTGTGAGCTGCG 175
QY 194 AGCCGAGTCCAGAGCTTGAAGCTTCCACGCGAGGCTCTGTTGCGCAGCGTGGAGCTCA 253
Db 176 AGCCGAGTCAAGAGCTTGAAGCTTCCACGCGAGGCTCTGTTGCGCAGCGTGGAGCTCA 235
QY 254 GCGTGTCCCAAGCGCGCGCGCGGAGGCGCGAGCAAGAGGAGGCTCGGCGCGG 313
Db 236 GCGTGTCCCAAGCGCGCGCGCGGAGGCGCGAGCAAGAGGAGGCTCGGCGCGG 295
QY 314 ACAGAGTGCACACAGCTCGCAGCGCGCGGCGAGGCGGCGCTCGAAGAGCCGAGAGG 373
Db 296 ACAGAGTGCACACAGCTCGCAGCGCGCGGCGAGGCGGCGGCTCGAAGAGCCGAGAGG 355
QY 374 CGAAGAGGCGCAAGAGAGAGCTGAGTCTGAGGAGGTGAGGCTCAAGATCGGCAACC 433
Db 356 CGAAGAGGCGCAAGAGAGAGCTGAGTCTGAGGAGGTGAGGCTCAAGATCGGCAACC 415
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QY 494 CGCCACTGGAAGCATGATCAGAGCGACCTGATGTTGGAGAGCTCCGCGCGCGCATCTTCAT 553
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QY 554 CCGGCGGTTTTCCGATGATCATGCGAGCGAGGAGGAGTCCGCGCTCTTTCGCGGCAACG 613
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QY 731 CGCTGATCGCGCGAGCGCTGCG-CGAGTGGCGTCAACCTGT--GCACCTATCCATGGA 788
Db 716 CGGTGTTGGCGGAGGCGTCTGCTCGAGAGTGGGCTTAACCTGTGACACTATCCATGGA 775
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QY 789 GC-TCGTCAAGACCCGCTTCCATCGAGA--GACGTGTACGACAACTCTTCCACGC 845
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QY 846 GTTTCGTCA 854
Db 836 GTTGTGTA 844
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RESULT 5

BO606434 655 bp mRNA linear EST 25-JUN-2002
LOCUS BRX 2295 wheat EST endosperm library Triticum aestivum cDNA 5',
mRNA sequence.

ACCESSION BO606434
VERSION BO606434.1 GI:21555728
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Triticum.

REFERENCE 1 (bases 1 to 655)
AUTHORS Clarke,B., Lambrecht,M. and Rhee,S.Y.
TITLE Arabidopsis genomic information for interpreting wheat EST
sequences
JOURNAL Punct. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE 22478026
PUBMED 12590341

COMMENT

Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rheeo@coma.stanford.edu.

FEATURES

Source Location/Qualifiers
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/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wynua"
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/tissue_type="endosperm"
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(days post anthesis)"
/clone_lib="wheat EST endosperm library"

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Best Local Similarity 99.8%; Pred. No. 8e-134;
Matches 645; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 GCGGCGGTCCTTAGAGTCCGCTTCTTGGAGTCCACAGCCGAGTCCAGAGCTTGA 60
QY 216 CTTCCACGAGAGGCTCGTTTCGCGAGGTGAGACTGAGCTGTCCACGCGCGCGCC 275
Db 61 CTTCCACGAGAGGCTCGTTTCGCGAGGTGAGACTGAGCTGTCCACGCGCGCGCC 120
QY 276 GGTAGCGGCGAGCATGACGGAAGGCTCGGCGCGCGAGCATGTCGACACAGCTGCG 335
Db 121 GGTAGCGGCGAGCATGACGGAAGGCTCGGCGCGCGAGCATGTCGACACAGCTGCG 180
QY 336 AGCCGCGGCGAGGCGGCGCTTCAGAAAGGCCCAAGAGCGCAAAAGGCGCAAGCGCA 395
Db 181 AGCCGCGGCGAGGCGGCGCTTCAGAAAGGCCCAAGAGCGCAAAAGGCGCAAGCGCA 240
QY 396 GCTAGCTTGAGGAAGGAGGTCAGATCGGCAACCGCACCTGCGCGCGCTGTGAG 455
Db 241 GCTAGCTTGAGGAAGGAGGTCAGATCGGCAACCGCACCTGCGCGCGCTGTGAG 300
QY 456 CGGCGCATCCGCGCGCGCTGTGAGAGACTTTCGTGCGCGCACTGAGAGCATCAGAGC 515
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Db      CGGCGCATCGCGCGCGCGCTGTCAGAGACTTTGTGGCGCACTGAGAGCATCAGAC 360
Qy      516 GCACCTGATGATGGAGAGCTCCGCGCGCGCACTCCATGCGCGGGTTTCCGGTGGATCAT 575
Db      361 GCACCTGATGATGGAGAGCTCCGCGCGCGCACTCCATGCGCGGGTTTCCGGTGGATCAT 420
Qy      576 GCGGACGAGAGGGGTGCGCGCGCTCTTCCGCGGCAAGCGCGTCAACGTCCTCGCGCGC 635
Db      421 GCGGACGAGAGGGGTGCGCGCGCTCTTCCGCGGCAAGCGCGTCAACGTCCTCGCGCGC 480
Qy      636 GCCAAGCAGAGCCATGAGACATTCCTTACGACACGCGGCAAGAGTACCTGACCCCGGA 695
Db      481 GCCAAGCAGAGCCATGAGACATTCCTTACGACACGCGGCAAGAGTACCTGACCCCGGA 540
Qy      696 GCGCGGAGAGCCAGCCAGGTCCCGCATCCCGCGCGCTGTGCGCGGAGCGCTCGCGG 755
Db      541 GCGCGGAGAGCCAGCCAGGTCCCGCATCCCGCGCGCTGTGCGCGGAGCGCTCGCGG 600
Qy      756 AGTGGCGTCAACCGCTGACCTATCCCATGAGAGCTGTGCAAGAC 801
Db      601 AGTGGCGTCAACCGCTGACCTATCCCATGAGAGCTGTGCAAGAC 646

RESULT 6
LOCUS   CV054670              710 bp      mRNA      linear      EST 24-AUG-2004
DEFINITION   BNE1124a Barley EST endospERM library Hordeum vulgare subsp.
              vulgare cDNA BNE1124a 5' similar to putative Brittle-1
              protein, chloroplast precursor, mRNA sequence.
ACCESSION   CV054670
VERSION     CV054670.1  GI:51517691
SOURCE      EST.
            Hordeum vulgare subsp. vulgare
            Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Hordeum.
            1 (bases 1 to 710)
REFERENCE   Ali, S., Holloway, B. and Taylor, W.C.,
            Normalisation of cereal endospERM EST libraries for structural and
            functional genomic analysis
            Plant Mol. Biol. Rep. 18, 123-132 (2000)
JOURNAL     Commonwealth Scientific and Industrial Research Organisation
            Division of Plant Industry.
            CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
            Tel: 61 2 6246 5223
            Fax: 61 2 6246 5000
            Email: Bill.Taylor@csiro.au
COMMENT     Seq primer: M13 reverse primer
            High quality sequence stop: 710.
            Location/Qualifiers
              1..710
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                /mol_type="mRNA"
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                /clone="BNE1124a"
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                /dev_stage="developing endospERM tissue 10, 12, 15 dpa
                (days post anthesis)"
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                was prepared from endospERM tissues of the barley cultivar
                Himalaya. cDNA was synthesised from pooled 10, 12, and 15
                dpa endospERM using Not I-oligo(dT)18 primer/adaptor
                (Pharmacia Biotech), and then ligated to the Sal I-Not I
                site of Ziplox vector (Life Technology) after adding a
                Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan
                Ali and Bill Taylor."

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ORIGIN
Query Match      39.4%; Score 640.6; DB 7; Length 710;
Best Local Similarity 94.7%; Pred. No. 7,8e-133;
Matches 674; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

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Qy      696 GCGCGGCGAGCCAGCCAGGTCCCATCCCGACGCGCTGTGCGCGGAGCGCTCGCGG 755
Db      61 GCGCGGCGAGCCAGCCAGGTCCCATCCCGACGCGCTGTGCGCGGAGCGCTCGCGG 120
Qy      756 AGTGGCGTCAACCGCTGTGACCTATCCCATGAGAGCTGTCAAAACCCGTTCACATCGA 815
Db      121 AGTGGCGTCAACCGCTGTGACCTATCCCATGAGAGCTGTCAAAACCCGTTCACATCGA 180
Qy      816 GAAGAGCTGTGACGACAACTCCTCCAGCGGTTGCTCAAGATGTTGCGGACGAGAGGCC 875
Db      181 GAAGAGCTGTGACGACAACTCCTCCAGCGGTTGCTCAAGATGTTGCGGACGAGAGGCC 240
Qy      876 GCGGAGCTGTACCGCGGCGTGGCGCGGACCTGATCGCGTGTGCTCCGTACCGCGGC 935
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Qy      936 CAACCTTCTACGCTTACGAGACGCTGCGCGCGCTGTACCGCGCGCTCGGGAAAGAGA 995
Db      301 CAACCTTCTACGCTTACGAGACGCTGCGCGCGCTGTACCGCGCGCTCGGGAAAGAGA 360
Qy      996 GGTGGGCAACGTCGCGGACGCTGATCGGGTCCGGGGGGGGCCATAGCCAGCACCGGC 1055
Db      361 GGTGGGCAACGTCGCGGACGCTGATCGGGTCCGGGGGGGGCCATAGCCAGCACCGGC 420
Qy      1056 CACGTTCCCGCTGAGAGTGGCGCGGAGAGATGACAGTGGCGCGCTGGCGGAGGCA 1115
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Db      481 GGTGTCAAGAACGTCGTCGACGCGCATGTACTGTCTCTCGACACAAAGAGGCCCGCGG 540
Qy      1176 GCTCTCCGCGGCGCTGGCGCGGCGGACGTCACGATCAAGCTCAGCGCGCGGATCTCTT 1235
Db      541 GCTCTCCGCGGCGCTGGCGCGGCGGACGTCACGATCAAGCTCAGCGCGGATCTCTT 600
Qy      1236 CATGTCTCTACGAGCGCTTGAAGAGATCTTGTGACGAGAAAGAGACGCGCGCGCG 1295
Db      601 CATGTCTCTACGAGCGCTTGAAGAGATCTTGTGACGAGAAAGAGACGCGCGCGCG 657
Qy      1296 CGAGCCCGAGAGAGAGACGAGACCGGACAGGACGAGAGACGCGCGCGCG 1347
Db      658 CGAGCCCGAGAGAGAGACGAGACCGGACAGGACGAGAGACGCGCGCGCG 709

RESULT 7
LOCUS   AM448382              787 bp      mRNA      linear      EST 03-JAN-2001
DEFINITION   BRY 646 BRY Triticum aestivum cDNA clone P40-2D, mRNA sequence.
ACCESSION   AM448382
VERSION     AM448382.1  GI:12018917
KEYWORDS    EST.
            Triticum aestivum (bread wheat)
SOURCE      Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Triticum.
            1 (bases 1 to 787)
REFERENCE   Clarke, B.C., Hobbs, M. and Apple, R.,
            Genes active in developing wheat endospERM
            Unpublished (2000)
JOURNAL     Division of Plant Industry
COMMENT     Contact: Bryan Clarke

```

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GPO Box 1600, Canberra, ACT, Australia
Tel: 61 2 6246 5054
Fax: 61 2 6246 5000
Email: bryan@p1.csiro.au.

FEATURES

source

Location/Qualifiers
1. .787

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ORIGIN

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Best Local Similarity 93.7%; Pred. No. 1.3e-132;
Matches 688; Conservative 0; Mismatches 44; Indels 2; Gaps 2;

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DB 61 AATGGCCGCGAGCAATGTGTGACCAAGAACACCGCGCTCGCTGTATGACAAGAA 120
QY 144 GAACTGTTATTGCGGCGGCTCCTGAGGTGCGCTTCCCTTGGAGCTTGCAGCCGAGTC 203
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QY 204 CAGAGCTTGGACTTCCAGCAGGAGGCTGTGTGGCAGCGTGGGACTCAGCTGTCCA 263
DB 181 CAGAGCTTGGACTTCCAGCAGGAGGCTGTGTGGCAGCGTGGGACTCAGCTGTCCA 240
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QY 324 ACACCACTTCGAGCGCGCGGCGAGGCGGCGTCCAGAAAGGCCAGAAAGGCC 383
DB 301 ACACCACTTCGAGCGCGCGGCGAGGCGGCGTCCAGAAAGGCCAGAAAGGCC 360
QY 384 CAAAAGAGAGAGCTGAGTCTGAGAGAGGTGAGAGGTCAAGATCGGCAACCGGCACTTGC 443
DB 361 CAAAAGAGAGAGCTGAGTCTGAGAGAGGTGAGAGGTCAAGATCGGCAACCGGCACTTGC 420
QY 444 GCGGCTGTGACGCGCGCATGCGCGCGCGTGTGAGGACTTTCGTGCGGCACTTGA 503
DB 421 GCGGCTGTGACGCGCGCATGCGCGCGCGTGTGAGGACTTTCGTGCGGCACTTGA 480
QY 504 GACGATCAGAGCGCATCTGATGTGGGAGCTTCGCGCGCGCATCTCATGCGCGGGTTT 563
DB 481 GACGATCAGAGCGCATCTGATGTGGGAGCTTCGCGCGCGCATCTCATGCGCGGGTTT 540
QY 564 CCGGTGATCATGCGGAGCGGAGGGTGGCCCGGCTCTTCGCGGCGCAACCGCTCAAGT 623
DB 541 TCGGTGATCATGCGGAGCGGAGGGTGGCCCGGCTCTTCGCGGAGCGCGTCAAGT 600
QY 624 CTTCCGCTGCGGCGCAAGGAGGCTATGAGG-ACCTTCACTTACAGACGCGGAGAAAGT 682
DB 601 CTTCCGCGGCGCGCGCAAGGAGGCTATGAGGACTTTCATTAAGACGCGGAGAAAGG 660
QY 683 ACCTGACCCCGAGGCG-CGCGAGGCGAGCGCAAGGTCCCATGCCAGCGCGCTGTGCGC 741
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DB 721 CGGAGCTTTCGCG 734

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RESULT 8

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LOCUS B0609766
DEFINITION BRY_646 wheat EST endosperm library Triticum aestivum CDNA 5', mRNA
sequence.

ACCESSION

B0609766
B0609766
B0609766.1 GI:21559105

VERSION

EST.
Triticum aestivum (bread wheat)

KEYWORDS

Triticum aestivum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE

1 (bases 1 to 787)
Clarke, B., Lambrecht, M. and Rhee, S.Y.

AUTHORS

Arabidopsis genomic information for interpreting wheat EST
sequences

TITLE

func. Integr. Genomics 3 (1-2), 33-38 (2003)

JOURNAL

22478026
12590341

MEDLINE

Contact: Lambrecht M
The Arabidopsis Information Resource

PUBMED

Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhe@acoma.stanford.edu.

FEATURES

Location/Qualifiers
1. .787

/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wyna"
/db_xref="taxon:4565"
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(days post anthesis)"
/clone_lib="wheat EST endosperm library"

ORIGIN

Query Match 39.4%; Score 639.6; DB 5; Length 787;
Best Local Similarity 93.7%; Pred. No. 1.3e-132;
Matches 688; Conservative 0; Mismatches 44; Indels 2; Gaps 2;

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QY 24 GAAGAACTCTAGGAGGAGGCACTATCAGTTCTGTCTTCCGAGATGGGGGGC 83
DB 1 GAAGAACTCTAGGAGGAGGCACTATCAGTTCTGTCTTCCGAGATGGGGGGC 60
QY 84 AATGGCCGCGAGCAATGTGTGACCAAGAACACCGCGCTCGCTGTATGACAAGAA 143
DB 61 AATGGCCGCGAGCAATGTGTGACCAAGAACACCGCGCTCGCTGTATGACAAGAA 120
QY 144 GAACTGTTATTGCGGCGGCTCCTGAGGTGCGCTTCCCTTGGAGCTTGCAGGCCGAGTC 203
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QY 204 CAGAGCTTGAAGCTTCCAGCAGAGGCTGTTCGCGAGGAGGACTCAGCTGTGCCA 263
DB 181 CAGAGCTTGAAGCTTCCAGCAGAGGCTGTTCGCGAGGAGGACTCAGCTGTGCCA 240
QY 264 CGGCGCCCGCGGTAGGCGCGAGCATGACGGAAGGCTCGGCGCGCGAGCATGCTGC 323
DB 241 CGGCGCCCGCGGTAGGCGCGAGCATGACGGAAGGCTCGGCGCGCGAGCATGCTGC 300
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DB 301 ACACCACTTCGAGCGCGCGGCGAGGCGGCGTGTGAGGAGGCCAGAAAGGCC 360
QY 384 CAAAAGAGAGAGCTGAGTCTGAGAGAGGTGAGAGGTCAAGATCGGCAACCGGCACTTGC 443
DB 361 CAAAAGAGAGAGCTGAGTCTGAGAGAGGTGAGAGGTCAAGATCGGCAACCGGCACTTGC 420
QY 444 GCGGCTGTGACGCGCGCATGCGCGCGCGTGTGAGGACTTTCGTGCGGCACTGGA 503

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QY	206	GGAGCTTGAGACTTCCACGACGAGGCTCTGTTGCCAGCGCTGGGACTCAGCTCTGTCCACG	265
Db	181	GGAGCTTGAGACTTCCACGCAATGCTCTGTTGCCAGCGCTGGGACTCAGCTCTGTCCACG	240
QY	266	GGCGCCCGCGGTTAGCGGCGGAGCATGACGGGAAGCTTCGGCCCGCCGACGACCTGTGCAC	325
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QY	446	GGCTGTGTAGAGGGGGCCATTCGCCCGCGCCGCTGTGAGAGACTTTTGTGTGCGCCACTGTGAGA	505
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QY	506	CGATCAGGACGCACTGATGTGGTGGGAGACTCCGGCGCGGACCTCCATCGACCGCGGGTTTCC	565
Db	481	CGATCAGGACGCACTGATGTGGGAGACTTCGGCGCGGACCTCCATCGAGCGGGGTTTTTCC	540
QY	566	GGTGGATCATGCGGACGGAAGGGGTGGGCC--GGCCTCTTCCGCGGCAACGCCCTCAACGT	623
Db	541	GGTGGATCATGCGGACGGAAGGGGTGGGCCCGCGGCTCTTCCGCGGAAACGCCCTCAACGT	600
QY	624	CTTCCGCGTCCGCGCCAGCAGAGGCTCATGTGAGCATTTCACTTAACGACAGCGCGAAGAAAGTA	683
Db	601	CTTCCGCGTCCGCGCCAGCAGAGGCTCATGTGAGCATTTCACTTAACGACAGCGCGAAGAAAGTA	660
QY	684	CCTGACCCCGGAGGCGCGGCG 703	
Db	661	CCTTAAACCCCGGAGCGCGG 680	
RESULT 10			
AL506887			
LOCUS			
DEFINITION	AL506887 Hordeum vulgare Barke developing caryopsis (3..15.DAP)		
ACCESSION	AL506887		
VERSION	AL506887		
KEYWORDS	AL506887.1 GI:12033102		
SOURCE	EST.		
ORGANISM	Hordeum vulgare subsp. vulgare		
REFERENCE	Hordeum vulgare subsp. vulgare		
AUTHORS	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
TITLE	Plantae; Magnoliophyta; Liliopsida; Poales; Poaceae;		
JOURNAL	Plantae; Tricicase; Hordeum.		
COMMENT	1 (bases 1 to 700)		
	Michalek,W., Meschke,W., Pleisner,K.-P. and Graner,A.		
	EST sequencing and analysis in barley		
	Unpublished (2000)		
	Contact: Michalek W		
	Institute for Plant Genetics and Crop Plant Research		
	Corrensstr.3, D-06466 Gatersleben, Germany		
	Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de		
	Seq primer: T3 primer for 5' end.		
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 /lab_host="XLOLR"
 /clone_lib="Hordeum vulgare Barke developing caryopsis (3.-15.DAP)"
 /note="Vector: plasmid pBK-CMV, Site 1: EcoRI, Site 2: XhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb. Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'- and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp"

ORIGIN

Query Match 36.5%; Score 593.4; DB 1; Length 700;
 Best Local Similarity 92.0%; Pred. No. 3e-122;
 Matches 668; Conservative 0; Mismatches 29; Indels 29; Gaps 3;

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DB 2 CCTAGGCGGCGACGATACGATTCGTTGCTTCTCTGAGATGCGCGGCGCATGCGG 61
    |||||
OY 92 CGACGACATGATGATCAAGAACAAACGCGCTCGCTGATGAGACAAAGAACTGGT 151
    |||||
DB 62 CACGACATGATGATCAAGAACAAACGCGCTCGCTGATGAGACAAAGAACTGGT 121
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OY 152 TATTGCGGCGGATCCGTTGAGGTGCGCTTCCCTTGGAGTGCAGCCCGAGTCCAGAGCT 211
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DB 122 TCTTTGCGGCGGCGCTGAGGTGCGCTTCTCTTGGAGTCCAGCCCGAGTCCAGAGCT 181
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OY 212 TGGACTTCCACGCGAGGCTCTGTTCCGACAGTGGAGCTAGGCTGTGCCAGCGCGCC 271
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DB 182 TGGAGTTCCACGCGAGGCTCTGTTCCGACAGTGGAGCTAGGCTGTGCCAGCGCGCC 234
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OY 272 CGCGCGTAGCGCGAGATGACGCGGAGAGCTCGGCGCGCGAGACGCTCGCACACCGC 331
    |||||
DB 235 -----GACGGAGAGGCTCGGCGCGCGCGAGACGCTCGCACACCGC 274
    |||||
OY 332 TCGCAGCGCGCGGCGAGGCGGCGCTCCAGAAAGCCAGAAAGCGAAGAAAGCCAAAGAGC 391
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DB 275 TCGCAGCGCGCGGCGAGATGCGGCGCTCCAGAGCGCCAGAAAGCGAAGAAAGCCAAAGAGC 334
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OY 392 AGCAGCTAGTCTGAGGAAGTGAAGGTCAAGATGCGCAACCCGACCTGCGGCGGCTGG 451
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DB 335 AGCAGCTAGTCTGAGGAAGTGAAGGTCAAGATGCGCAACCCGACCTGCGGCGGCTGG 394
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OY 452 TCAGGCGGCGCATGCGCGGCGCGCTGTCAGAGGACTTGTGAGCGCACTGGAGAGCATCA 511
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DB 395 TCAGGCGGCGCATGCGCGGCGCGCTGTCAGAGGACTTGTGAGCGCGCTGGAGAGCATCA 454
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OY 512 GAGCAGCACTGATGATGAGGAGGAGCTCCGCGCGCATCCATGAGCCGAGGCTTTTCGGTGA 571
    |||||
DB 455 GAGCAGCACTGATGATGAGGAGGAGCTCCGCGCGCATCCATGAGGCGGAGGCTTTTCGGTGA 514
    |||||
OY 572 TCATTCGAGCGAGAGGAGGAGCTTCCTTCGCGGCGCAAGCGCTCAAGCTCTCCGCG 631
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DB 515 TCATTCGAGCGAGAGGAGGAGCTTCCTTCGCGGCGCAAGCGCTCAAGCTCTCCGCG 574
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DB 575 TCGCGCCCAAGAGGCGCATTCAGACCTTCACTTGAAGACGCGGAGAAAGTAACTGAGACC 634
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OY 692 CGAAGG-CGCGGAGCGAGCAAGGTCCCATCCCAAGCGCGCTGTCGCGG-AGCGCT 749
    |||||
DB 635 CGAAGGCGCGGAGCGAGCAAGGTCCCATCCCAAGCGCGCTGTCGCGGAGCGCT 694
    |||||
OY 750 CGCGCG 755
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DB 695 CGCGCG 700
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RESULT 11

AL507153 700 bp mRNA linear EST 04-JAN-2001
 AL507153 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)

LOCUS

Hordeum vulgare subsp. vulgare cDNA clone HY05M09T 5', mRNA
 sequence.

ACCESSION

AL507153 GI:12033368

VERSION

EST.

KEYWORDS

Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.

SOURCE

1 (bases 1 to 700)

REFERENCE

Michalek, W., Meschke, W., Pleisner, K.-P. and Graner, A.

AUTHORS

EST sequencing and analysis in barley

TITLE

Unpublished (2000)

JOURNAL

Contact: Michalek W

COMMENT

Institute for Plant Genetics and Crop Plant Research
 Corrensstr. 3, D-06466 Gatersleben, Germany
 Email: michalek@ipk-gatersleben.de, http://ipkrc.ipk-gatersleben.de
 Seq primer: T3 primer for 5' end.
 Location/Qualifiers

1. 700

FEATURES

/organism="Hordeum vulgare subsp. vulgare"

source

/mol_type="mRNA"

cultivar="barke"

/sub_species="vulgare"

/db_xref="taxon:112509"

/clone="HY05M09T"

/tissue_type="developing caryopsis (3.-15.DAP)"

/lab_host="XLOLR"

/clone_lib="Hordeum vulgare Barke developing caryopsis (3.-15.DAP)"

/note="Vector: plasmid pBK-CMV, Site 1: EcoRI, Site 2: XhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb. Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'- and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp"

ORIGIN

Query Match 36.4%; Score 592.2; DB 1; Length 700;
 Best Local Similarity 92.0%; Pred. No. 5.5e-122;

Matches 668; Conservative 0; Mismatches 29; Indels 29; Gaps 3;

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OY 22 CTGAAGAACTCTAAGGAGGACGATATCA-GTTGTGTTCTTCTCTCGAATGCGCGC 80
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    |||||
OY 81 GGCATATGCGCGACGACATGATGATGACCAAGAACCCGCGCTCGCTGATGAGCA 140
    |||||
DB 62 GGCATATGCTGCAACGACATGATGATGACCAAGAACCCGCGCTCGCTGATGAGCA 121
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OY 141 GAAGAACTGTTATTGAGCGCGGAGTCCCTGAGTTCCTTCTGAGAGCTCGAGCGCGCA 200
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DB 122 GAAGAACTGTTATTGAGCGCGGAGTCCCTGAGTTCCTTCTGAGAGCTCGAGCGCGCA 181
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OY 201 GTCCAGAGGTTGAGACTTCCACGACAGGCTCTGTTCCAGAGTGGAGACTAGCTGTG 260
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DB 182 GTCCAGAGGTTGAGACTTCCACGACAGGCTCTGTTCCAGAGTGGAGACTAGCTGTG 241
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OY 261 CCACGAGCGCGCGCGGATGACGAGCATGACGGAAGGCTCGCGCGCGCGACGACGCT 320
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DB 242 CCAC-----GACGGAGAGGCTCGCGCGCGCGACGACGCT 274
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QY 321 CGCACACACCTGCGACGCGCGGCGGAGCGGCGGCTCCAGAGAGCCCAAGAGGCGAAGAAA 380
 Db 275 CGCACACCAACTGCGACGCGCGGCGGAGTGCGGGCGCTCAGAGAGCCCAAGAGGCGAAGAAA 334
 QY 381 GGGCAAAAACAGAGAGCTGAGTCTGAGAGAGGTAGAGGTCAAGATCGGCAACCCGCACT 440
 Db 335 GGGCAAGAAACAGAGTGGGTCTGAGAGAGGTAGAGGTCAAGATCGGCAACCCGCACT 394
 QY 441 GCGGCGGCTGATGAGCGGCGGCGCATCGCGGCGGCTTCGAGAGCTTCGAGGCGGCACT 500
 Db 395 GCGTGGCTGATGAGCGGCGGCGCATCGCGGCGGCTTCGAGAGCTTCGAGGCGGCACT 454
 QY 501 GGAAGACATCAGAGCGACCTGATGATGAGAGAGTCCGCGCGCGCATTCATGAGCGGCGGT 560
 Db 455 GGAAGACATCAGAGCGACCTGATGATGAGAGAGTCCGCGCGCGCATTCATGAGCGGCGGT 514
 QY 561 TTTCCGGTGTATCATGCGGACGAGAGGAGTGGCGGCGGCTCTT-CCGCGCGCAAGCGGCTCA 619
 Db 515 TTTCCGGTGTATCATGCGGACGAGAGGAGTGGCGGCGGCTCTTCCGCGCGCAAGCGGCTCA 574
 QY 620 ACCTGCTCCGCGTCCGCGCAAGAGGCGATTCAGAGCTTCATTCAGAGAGCGGCGAAGA 679
 Db 575 ACCTGCTCCGCGTCCGCGCAAGAGGCGATTCAGAGCTTCATTCAGAGAGCGGCGAAGA 634
 QY 680 AGTACTGACCCCGAGAGCGCGCGAGCGCAGCAGAGTCCCATCCCGCGCGGCTCGTGC 739
 Db 635 AGTACTGACCCCGAGAGCGCGCGAGCGCAGCAGAGTCCCATCCCGCGCGGCTCGTGC 694
 QY 740 CCGGAG 745
 Db 695 CCGGAG 700

RESULT 12
 LOCUS AL506597 700 bp mRNA linear EST 04-JAN-2001
 DEFINITION AL506597 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
 Hordeum vulgare subsp. vulgare cDNA clone HY03K09T 5', mRNA
 sequence.
 ACCESSION AL506597
 VERSION AL506597.1 GI:12032812
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 1 (bases 1 to 700)
 Michael, W., Weschke, W., Pleisner, K.-P. and Graner, A.
 EST sequencing and analysis in barley
 unpublished (2000)
 CONTACT: Michael W
 Institute for Plant Genetics and Crop Plant Research
 Corrensstr. 3, D-06466 Gatersleben, Germany
 Email: michael@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
 Seq primer: T3 primer for 5' end.
 Location/Qualifiers
 1..700
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="barke"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
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 /issue_type="developing caryopsis (3.-15.DAP)"
 /lab_host="XLOLR"
 /clone_lib="Hordeum vulgare Barke developing caryopsis
 (3.-15.DAP)"
 /note="Vector: plasmid pBK-CMV; Site_1: EcoRI, Site_2:
 XhoI; mRNA was made from developing caryopsis (3.-15.DAP)
 of spring barley variety 'Barke', a high quality malting
 variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI
 (3'-end of cDNA). NOTE: Due to a cloning artefact caused

ORIGIN

by the kit, in most cases the EcoRI site is NOT present,
 as well as the EcoRI adapter. Average insert size is 1 kb
 Sequence trimming: Vector sequences and sequence ends were
 trimmed from the 5'- and 3'-end until a 50 bp window
 contains less than two ambiguities. The maximum length was
 set to 700 bp"

Query Match 35.6%; Score 577.8; DB 1; Length 700;
 Best Local Similarity 89.9%; Pred. No. 9,4e-119;
 Matches 653; Conservative 0; Mismatches 43; Indels 30; Gaps 2;

QY 8 GAGGAGTGAAGAGTGAAGAACTCTTGAAGAGGAGGACGATATGATCTTCTGCTTCC 67
 Db 1 GAGGAGTGAAGAGTGAAGAACTCTTGAAGAGGAGGACGATATGATCTTCTGCTTCC 60
 QY 68 TCGAGATGAGCGGCGGCGCAATGCGCGAGCGAAGTGTGACCAAGAACACCGCGCTCGC 127
 Db 61 TCGAGATGAGCGGCGGCGCAATGCGCGAGCGAAGTGTGACCAAGAACACCGCGCTCGC 120
 QY 128 TCGTCAATGACCAAGAAAGACTGTTATGCGCGCGGCTTCTTGAAGTGTGCTTCTTGA 187
 Db 121 TCGCCTATGACCAAGAAAGACTGTTATGCGCGCGGCTTCTTGAAGTGTGCTTCTTGA 180
 QY 188 GCTGCGAGCGCGGAGTCCAGAGGCTTGAAGTTCACAGAGGCTTGTGCGCGAGCGTGG 247
 Db 181 GCTGCGAGCGCGGAGTCCAGAGGCTTGAAGTTCACAGAGGCTTGTGCGCGAGCGTGG 240
 QY 248 GACTCAGCTGTGTCACAGCGGCGCGCGCGGAGCGCGAGCATGACGGAAGGCTTGGC 307
 Db 241 GACTCAGCTGTGTCACAGCGGCGCGCGCGGAGCGCGAGCATGACGGAAGGCTTGGC 273
 QY 308 CCGCGCGACGACGCTGCGACACCAAGCTGCGACGCGCGCGGCGGAGCGGCTGCAAGAGCCC 367
 Db 274 CCGCGCGACGACGCTGCGACACCAAGCTGCGACGCGCGCGGCGGAGCGGCTGCAAGAGCCC 333
 QY 368 AGAAGCGAAGAAAGGCGCAAGAGAGGAGTGTGAGTGTGAGAGAGTGTGAGAGTGTG 427
 Db 334 AGAAGCGAAGAAAGGCGCAAGAGAGGAGTGTGAGTGTGAGAGAGTGTGAGAGTGTG 393
 QY 428 GCAACCGGACCTGCGCGGCGGCTGTCAGCGGCGGCAATGCGCGGCGGCTGTCAGAGACTT 487
 Db 394 GCAACCGGACCTGCGCGGCGGCTGTCAGCGGCGGCAATGCGCGGCGGCTTTCAGAGACTT 453
 QY 488 TCGTGGCGGACCTGTCAGAGAGTATGAGAGCGACCTGATGTTGGAGAGTCCGCGCGGACT 547
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 QY 548 CCAATGCGCGGCGGCTTCCGCTGATCATGCGGAGCGAGAGGAGTGGCGCGGCTTTCGCGG 607
 Db 514 CCAATGCGCGGCGGCTTCCGCTGATCATGCGGAGCGAGAGGAGTGGCGCGGCTTTCGCGG 573
 QY 608 GCAACCGGCTCAAGCTCTCCGCGTGCAGCGCAAGAGGCGATTCAGAGACTTCACTTACG 667
 Db 574 GCAACCGGCTCAAGCTCTCCGCGTGCAGCGCAAGAGGCGATTCAGAGACTTCACTTACG 633
 QY 668 ACAAGCGGCAAGAAAGTACTT---GACCCCGAGAGGCGCGCGAGCGCAAGAGTCCCATTC 724
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 Db 694 TCCTCC 699

RESULT 13
 LOCUS CD433626 897 bp mRNA linear EST 03-JUN-2003
 DEFINITION EL01N0313C10.b Endosperm_3 Zea mays cDNA, mRNA sequence.
 ACCESSION CD433626
 VERSION CD433626.1 GI:31349269
 KEYWORDS EST.
 SOURCE Zea mays

Oy		988 - -AAAGAGGAGTGGGGCAACGTCCCGAAGCTGCATCGGGTCGCGCGGCGCCACTAG	1045
Db		714 CCGCGCGGAGACGTGGGCCCGCGTGACGCTGCTCATCGGGTCCGCGCGGCGCCACTCG	773
Oy		1046 CCAGCAGCGGCACAGTTCCCGCTGGAGGTGGCGCGGAAGCAGATGACAGTGGCGCCGTGG	1105
Db		774 CCAAGCTCGGCGACGGTTCGCGTAGAGGTGGCCGCAAGCAGATGACAGTGGCGCTTGG	833
Oy		1106 GCGGAGGCGAGGTGTACAAGAAGTGTGCAGCCCATGTACTCTGCATCTCGAAGAAGAGG	1165
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Oy		1166 GCAC 1169	
Db		894 GCgc 897	
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RESULT 14			
BE413774			
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DEFINITION		SCU002.H05.R990714 ITFC SCU wheat Endosperm Library Triticum aestivum cDNA clone SCU002.H05, mRNA sequence.	
ACCESSION		BE413774	
VERSION		BE413774.1	GI:9411620
KEYWORDS		EST.	
SOURCE		Triticum aestivum (bread wheat)	
ORGANISM		Triticum aestivum	
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
AUTHORS		Poideae; Triticeae; Triticum.	
		1 (bases 1 to 784)	
		Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Hermann,R.G., Holton,T., Jacquemlin,J.M., Jia,J., Jouderir,P., Langridge,P., Izzo,G.R., Lin,J.D., McGuire,P., Ogihara,Y., Pecchioni,N., Qualest,C., Schuch,W., Selvaraj,G., Sharifion,M., Sorrelle,M., Warburton,M. and Wenzel,G., International Triticaceae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticaceae Unpublished (2000)	
JOURNAL COMMENT		Contact: Holton T Centre for Plant Conservation Genetics, Southern Cross University PO Box 157, Lismore NSW 2480 AUSTRALIA Tel.: 61 2 6620 3409 Fax: 61 2 6622 2080 Email: tholton@scu.edu.au International Triticaceae EST Cooperative (ITEC) http://wheat.pw.usda.gov/genome . Location/Qualifiers	
FEATURES		Source	
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Best Local Similarity		94.7%; Pred. No. 1,4e-114;	
Matches 627; Conservative 0; Mismatches 28; Indels 7; Gaps 5;			
Oy		156 GCGGCGGTCCTTAGAGTCGCTTCCCTTGGAGCTCCAGCCGAGTCCAGGACTTGA	215
Db		125 GCGGCGGTCCTTAGAGTCGCTTCCCTTGGAGCTCCAGCCGAGTCCAGGACTTGA	184
Oy		216 CTTCACACGACGAGGCTCGTTTCGCGCACGTGGAGCTACAGCTGTCCACGCGCGCC	275
Db		185 CTTCACACGACGAGGCTCTGTTCGCGCACGTGGAGCTACAGCTGTCCACGCGCGCC	244

	RESULT 15				
	CK125192				
LOCUS		739 bp	mRNA	linear	EST 01-MAR-2004
DEFINITION	BE51824106P15 BE51824 Hordeum vulgare subsp. vulgare cDNA clone				
ACCESSION	MPMG2010P156 5-PRIME, mRNA sequence.				
VERSION	CK125192				
KEYWORDS	CK125192.1	GI:44808194			
ORGANISM	EST.				
SOURCE	Hordeum vulgare subsp. vulgare				
	Hordeum vulgare subsp. vulgare				
	Eukaryota; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
	Poodeae; Triticeae; Hordeum.				
	1 (bases 1 to 739)				
REFERENCE	Kriemer,A., Fellner,T., Posselng,A., Radchuk,V., Weschke,W.,				
AUTHORS	Buerkle,L. and Kersten,B.				
TITLE	Application of the protein microarray technology for the				
	identification of expression library derived target proteins for				
	barley protein kinases CK2				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Birgit Kersten* and Winfriede Weschke**				
	*Plant Protein Chip Group, Department Lehrnach, **Department				
	Molecular Genetics, Gene Expression Group				
	*Max-Planck-Institute for Molecular Genetics, **Institute of Plant				
	Genetics and Crop Plant Research Gatersleben				
	*Innestr. 73 , D-14195 Berlin, Germany, **Corrensstrasse 3, D-06466				
	Gatersleben, Germany				
	Tel.: **49(0)30/84131648, **49(0)394825500				
	Fax: **49(0)30/84131128, **49(0)394825237				
	Email: *kersten@molgen.mpg.de, **weschke@ipk-gatersleben.de				
	Insert Length: 739 Std Error: 0.00				
	Plate: 6 row: p column: 15				

FEATURES	Seq primer: pQ85.	Location/Qualifiers
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	/lab_host="E. coli, SCS-1/PSR11"	
	/clone_id="BES1824"	
	/note="Vector: pQE30NST (AF074376); Site 1: SalI; Site 2: NotI; 0-10 DAF (days after flowering), cDNA synthesis using Pbluescript II XR cDNA-library construction kit (Stratagene) with an oligo(dT)-primer containing NotI restriction site and a SalI adapter (Invitrogen). The main library of 21500 clones was retrayed into the sublibrary BES 1824 containing 4100 putative expression clones. Note: Due to a cloning artefact caused by the kit, in most cases the SalI site is NOT present, as well as the SalI Adapter used for cloning. To excise the insert, restriction sites upstream SalI should be used (e.g. BamHI). Average insert size is 1 kb. Library generation and sequencing was granted in context of GABI; data are also accessible at https://gabi.rzpd.de "	
ORIGIN		
Query Match	34.2%	Score 555.6; DB 7; Length 739;
Best Local Similarity	90.4%	Pred. No. 9e-114;
Matches 643; Conservative	0; Mismatches 50; Indels 18; Gaps 4;	
QY	781	CCCATGAGCTCGTCGACAGACCCCGTCTACCTCGAGAAAGACGTGTACGAACTCTCTC 840
DB	17	CCCATGAGCTCGTCGACAGACCCCGTCTACCTCGAGAAAGATGTGTACGAACTCTCTC 76
QY	841	CACCGCTTCGTCAGAGATCGTSCGAGCAGAAAGCCCGGGGGAGCTGTACCGCGGCTGGCG 900
DB	77	CACCGCTTCGTCAGAGATCGTSCGAGCAGAAAGCCCGGGGGAGCTGTACCGCGGCTGGCG 136
QY	901	CCGAGCTGTATCGCGGTGTGTCGCGTACGCGGCGGCAACTTCTACGCTTACGAGACGCTG 960
DB	137	CCGAGCTGTATCGCGGTGTGTCGCGTACGCGGCGGCAACTTCTACGCTTACGAGACACTG 196
QY	961	CGCGGCTGTATCGCGCGCGCGTCTCGGGGAAAGAGAGTGTGGCAACGTCTCCGACCTGCTG 1020
DB	197	CGCGGCTGTATCGCGCGCGCGTCTCGGGGAAAGAGAGTGTGGCAACGTCTCCGACCTGCTG 256
QY	1021	ATCGGGGTCCGCGGGGGGGCCCATGAGCCAGACCGGCACTTCGCGCTGGAGATGTGGCGGG 1080
DB	257	ATCGGGGTCCGCGGGGGGGCCCATGAGCCAGACCGGCACTTCGCGCTGGAGATGTGGCGGG 316
QY	1081	AAGCAGATGACGATGTGGGCGCCGTGGGCGGAGAGAGGTGTACAAAGAACTGTCTCAGCGC 1140
DB	317	AAGCAGATGACGATGTGGGCGCCGTGGGCGGAGAGAGGTGTACAAAGAACTGTCTCAGCGC 376
QY	1141	ATGTATCTGATCTCTCGAGAGAGAGGACCGCGGGGCTTACCGCGGGCTTGGCGCCCAAGC 1200
DB	377	ATGTATCTGATCTCTCGAGAGAGAGGACCGCGGGGCTTACCGCGGGCTTGGCGCCCAAGC 436
QY	1201	TGCATCAAGCTCATAGCCCGCGCGGCACTTCTTCATGTGTCTACAGAGCTTGCAGAGAG 1260
DB	437	TGCATCAAGCTCATAGCCCGCGCGGCACTTCTTCATGTGTCTACAGAGCTTGCAGAGAG 496
QY	1261	ATTACTTGTGACGAGAAAGAGACGCGCGCGCCGCGCGAGGCCCGAGAGAGACCGAGACC 1320
DB	497	ATTACTTGTGACGAGAAAGAGACGCGCGCGCCGCGCGAGGCCCGAGAGAGACCGAGACC 553
QY	1321	GGAACGAGGAGAGACAGCGCGCGCCCAAGAG-----CTGAAACGGTATCGGCATGA 1374
DB	554	GGAACGAGGAGAGACAGCGCGCGCCCAAGAGAG-----CTGAAACGGTATCGGCATGA 613

QY 1375 ACTGATGAAGA-----TTATGGGACCGCTAAATCAGAAAGAAAATCGCGATTT 1426

Db 614 ACGGATCGAGGAACATTATGANTGTTACCGCTCAATATCAGAAAGAAAATCGCGATCT 673

QY 1427 GAATTTTGAAGCTAGACCTATTGCGATTTGAATCCTAAGCGGAAGTG 1477

Db 674 GGAA-TTTTCAAGTGTAAAGCTACCGCAATTGAATCTTAAAGAGGAAAGAG 723

Search completed: May 25, 2005, 12:24:38
Job time : 8074 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 04:44:09 ; Search time 1311 Seconds
(without alignment)
7337.589 Million cell updates/sec

Title: US-10-659-199-17

Perfect score: 1625

Sequence: 1 ggcacgtcagggagtggaag.....aaaaaaaaaaaaaaaaaaaaa 1625

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneeqn1980s:*\n2: geneeqn1990s:*\n3: geneeqn2000s:*\n4: geneeqn2001s:*\n5: geneeqn2001bs:*\n6: geneeqn2002as:*\n7: geneeqn2002bs:*\n8: geneeqn2003as:*\n9: geneeqn2003bs:*\n10: geneeqn2003cs:*\n11: geneeqn2003ds:*\n12: geneeqn2004as:*\n13: geneeqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	673.4	41.4	675	12	Ad142967 Plant CDN
2	672.6	41.4	1213	12	Ad140023 Plant CDN
3	549	33.8	698	12	Ad141898 Plant CDN
4	539.4	33.2	640	12	Ad142968 Plant CDN
5	511	31.4	661	12	Ad142969 Plant CDN
6	440.4	27.1	1056	12	Ad142974 Plant CDN
7	400.2	24.6	1267	2	Aaz20025 Wheat brl
8	397.6	24.5	1140	10	Aaz57636 Rice grai
9	392.6	24.2	449	2	Aaz20024 Wheat brl
10	361.6	22.3	1099	12	Ad142975 Plant CDN
11	357.8	22.0	1331	3	AAC49806 Arabidops
12	357.8	22.0	1334	3	AAC35455 Arabidops
13	256.8	15.8	653	3	Ad142973 Plant CDN
14	253.8	15.6	829	3	AAC49805 Arabidops
15	241.4	14.9	829	3	AAC34062 Arabidops
16	222.4	13.7	654	12	Ad144581 Plant CDN
17	179	11.0	580	2	Aaz20023 Soybean b
18	132	8.1	523	12	Ad144164 Plant CDN
19	129.8	8.0	285	6	ABL73796 Corn tass
20	127	7.8	3334	8	ACD45177 Human sec

21	125.4	7.7	1481	3	AAC76538 Human ORF
22	125.4	7.7	3337	4	Aa159228 Human pol
23	125.4	7.7	3333	3	Aa65058 Membrane-
24	125.4	7.7	3334	4	AaF92086 Human PRO
25	125.4	7.7	3334	5	AaF44204 Human PRO
26	125.4	7.7	3334	6	Ab874406 Human CDN
27	125.4	7.7	3334	6	ACA64351 Novel hum
28	125.4	7.7	3334	8	ACA91192 Novel hum
29	125.4	7.7	3334	8	ACD81569 Human CDN
30	125.4	7.7	3334	8	ACA60391 Novel hum
31	125.4	7.7	3334	8	ACA58838 CDNA enco
32	125.4	7.7	3334	8	ACA64014 CDNA enco
33	125.4	7.7	3334	8	ACA91278 CDNA enco
34	125.4	7.7	3334	8	ABX80810 Human sec
35	125.4	7.7	3334	8	ACD44319 CDNA enco
36	125.4	7.7	3334	8	ACA93725 Human CDN
37	125.4	7.7	3334	8	ACA67299 CDNA enco
38	125.4	7.7	3334	8	ACH66272 Novel hum
39	125.4	7.7	3334	8	ABX79490 Human sec
40	125.4	7.7	3334	8	ACA93511 Novel hum
41	125.4	7.7	3334	8	ABX81193 Novel hum
42	125.4	7.7	3334	8	ACD02326 Novel hum
43	125.4	7.7	3334	8	ACA89317 Novel hum
44	125.4	7.7	3334	8	ACA68954 Novel hum
45	125.4	7.7	3334	8	ACA93009 Novel hum

ALIGNMENTS

RESULT 1	
AD142967	
ID	AD142967 standard; CDNA; 675 BP.
XX	
AC	AD142967;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Plant CDNA #3967.
XX	
KW	Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW	soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW	maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW	stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW	plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
XX	antifungal.
XX	
OS	Eukaryota.
XX	
PN	US2004016025-A1.
XX	
PD	22-JAN-2004.
XX	
PF	26-SEP-2002; 2002US-00260238.
XX	
PR	26-SEP-2001; 2001US-0325277P.
PR	26-SEP-2001; 2001US-0325448P.
PR	04-APR-2002; 2002US-0370620P.
XX	
PA	(BUDM/) BUDMORTH P.
PA	(MOUG/) MOUGHAMER T.
PA	(BRIG/) BRIGGS S. P.
PA	(COOP/) COOPER B.
PA	(GLAZ/) GLAZEBROOK J.
PA	(GOFF/) GOFF S. A.
PA	(KATA/) KATAGIRI F.
PA	(KREP/) KREPS J.
PA	(PROV/) PROVART N.
PA	(RICK/) RICE D.
PA	(ZHUT/) ZHU T.
PI	Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F, Kreps J, Provart N, Rice D, Zhu T;

```
XX DR WPI; 2004-190374/18.
XX PT New rice promoter, useful for manipulating crop plants to alter or
XX PT improve phenotypic characteristics, e.g. produce large quantities of oil
XX PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX PT or high nutritional value.
XX PS Example 13; SEQ ID NO 3967; 230pp; English.
XX CC The invention relates to plant nucleotide sequences that direct seed-,
XX CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
XX CC or constitutive transcription of an operatively linked nucleic acid
XX CC segment. The invention also relates to a method for augmenting a plant
XX CC genome and a method of identifying a gene, where its expression is
XX CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
XX CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
XX CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
XX CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
XX CC encode are useful for manipulating crop plants to alter or improve
XX CC phenotypic characteristics, to produce large quantities of oil or
XX CC proteins, to incur resistance to insecticides, viruses or fungi, and to
XX CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
XX CC have a high nutritional value with reduced apical dominance or dwarfism,
XX CC early flowering or altered metabolic pathways. This sequence represents a
XX CC plant nucleic acid of the invention. Note: The sequence data for this
XX CC patent did not form part of the printed specification but was obtained in
XX CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 675 BP; 153 A; 176 C; 224 G; 122 T; 0 U; 0 Other;

Query Match      41.4%; Score 673.4; DB 12; Length 675;
Best Local Similarity 99.9%; Pred. No. 1.9e-119;
Matches 674; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 912 CGGCGTGTGTCGCTACGCGGCGGCCAACTTCTACGCTTACGAGACGCTGCGCGGTGTA 971
DB 1 CGGCGTGTGTCGCTACGCGGCGGCCAACTTCTACGCTTACGAGACGCTGCGCGGTGTA 60

QY 972 CCGCGCGCGCTCGGGGAAAGAGAGGTGGGCAAGTCCCGACGCTGCTGATCGGGTCCGC 1031
DB 61 CCGCGCGCGCTCGGGGAAAGAGAGGTGGGCAAGTCCCGACGCTGCTGATCGGGTCCGC 120

QY 1032 GGGGGGGGCGCATGCGCGACGCGGCAAGTCCCGTGGAGGTGGCGGGAAGCATGCA 1091
DB 121 GGGGGGGGCGCATGCGCGACGCGGCAAGTCCCGTGGAGGTGGCGGGAAGCATGCA 180

QY 1092 GGTGGGGCGCGTGGCGCGAGGCGAGTGTACAAAGACGTGTGACGCGCATGTACTGCAT 1151
DB 181 GGTGGGGCGCGTGGCGCGAGGCGAGTGTACAAAGACGTGTGACGCGCATGTACTGCAT 240

QY 1152 CCTCGAAGAGAGGGGACCGCGCGGCTGTACCGCGGGCTCGGCGCCCGAGTGCATCAAGCT 1211
DB 241 CCTCGAAGAGAGGGGACCGCGCGGCTGTACCGCGGGCTCGGCGCCCGAGTGCATCAAGCT 300

QY 1212 CATGCCGCGCGCGCGGCAATCTCTCATGTGCTACGAGGCGTGAAGAGATCTGTGCA 1271
DB 301 CATGCCGCGCGCGCGGCAATCTCTCATGTGCTACGAGGCGTGAAGAGATCTGTGCA 360

QY 1272 CGAAGAAAGAGACGCGCGCGCGCGAGCCCGAGAGAGACGAGACCGGACGAGGAG 1331
DB 361 CGAAGAAAGAGACGCGCGCGCGCGAGCCCGAGAGAGAGACGAGACCGGACGAGGAG 420

QY 1332 AGGACAGGCGCGCGCGCGCAAGAGCTGAACGGTGTGCGCATGAACCTAGATCAAGCATAT 1391
DB 421 AGGACAGGCGCGCGCGCGCAAGAGCTGAACGGTGTGCGCATGAACCTAGATCAAGCATAT 480

QY 1392 GGTGACCGTGAATTCGAAGAAAGAAATGCGTGAATTTGAATTTGAAGTGAAGCCCAT 1451
DB 481 GGTGACCGTGAATTCGAAGAAAGAAATGCGTGAATTTGAATTTGAAGTGAAGCCCAT 540

QY 1452 TGCATTTGAATCTTAAGCTGGAAGTGGCGCTTGAAGATTGAATTTGTTGTCAGG 1511
```

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DB 541 TGCATTTGAATCTTAAGCTGGAAGTGGCGCTTGAAGATTGAATTTGTTGTCAGG 600
QY 1512 AACATGCTCGTTTCAGTATAGCCGTGAATGATTTATGACACCTTCTGATCAATTC 1571
DB 601 AACATGCTCGTTTCAGTATAGCCGTGAATGATTTATGACACCTTCTGATCAATTC 660
QY 1572 AATAGAGAAAGAGTTC 1586
DB 661 AATAGAGAAAGAGTTC 675

RESULT 2
ADJ40023
ID ADJ40023 standard; cDNA; 1213 BP.
XX AC ADJ40023;
XX DT 06-MAY-2004 (first entry)
XX DE Plant cDNA #1023.
XX KW Plant; gene; seq; transcription; plant genome augmentation; cereal;
XX KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
XX KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
XX KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
XX KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
XX KW antifungal.
XX OS Burkaryota.
XX PN US2004016025-A1.
XX PD 22-JAN-2004.
XX PF 26-SEP-2002; 2002US-00260238.
XX PR 26-SEP-2001; 2001US-0325277P.
XX PR 26-SEP-2001; 2001US-0325448P.
XX PR 04-APR-2002; 2002US-0370620P.
XX PA (BUDW.) BUDWORTH P.
XX PA (MOUG.) MOUGHAMER T.
XX PA (BRIG.) BRIGGS S P.
XX PA (COOP.) COOPER B.
XX PA (GLAZ.) GLAZEBROOK J.
XX PA (GOF.) GOF S A.
XX PA (KAT.) KATAGIRI F.
XX PA (KREP.) KREPS J.
XX PA (PROV.) PROVART N.
XX PA (RICK.) RICHE D.
XX PA (ZHUT.) ZHU T.
XX PT Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
XX PT Goff SA, Katagiri F, Kreps J, Provart N, Riche D, Zhu T;
XX PS WPI; 2004-190374/18.
XX DR
XX PT New rice promoter, useful for manipulating crop plants to alter or
XX PT improve phenotypic characteristics, e.g. produce large quantities of oil
XX PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX PT or high nutritional value.
XX PS Claim 25; SEQ ID NO 1023; 230pp; English.
XX CC The invention relates to plant nucleotide sequences that direct seed-,
XX CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
XX CC or constitutive transcription of an operatively linked nucleic acid
XX CC segment. The invention also relates to a method for augmenting a plant
XX CC genome and a method of identifying a gene, where its expression is
XX CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
XX CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
XX CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
XX CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
```

CC encode are useful for manipulating crop plants to alter or improve
 CC phenotypic characteristics, to produce large quantities of oil or
 CC proteins, to incur resistance to insecticides, viruses or fungi, and to
 CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
 CC have a high nutritional value with reduced apical dominance or dwarfism,
 CC early flowering or altered metabolic pathways. This sequence represents a
 CC plant nucleic acid of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification but was obtained in
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1213 BP; 191 A; 419 C; 438 G; 165 T; 0 U; 0 Other;

Query Match 41.4%; Score 672.6; DB 12; Length 1213;

Best Local Similarity 82.3%; Pred. No. 2.9e-119;

Matches 825; Conservative 0; Mismatches 164; Indels 14; Gaps 4;

QY 291 TGACGGGAAGGCTGGCGCCGCGACGACGTCGACACGACTTCGACGCCG----- 341
 DB 155 TCGGCGAAGGGCGCGGACCACTGCGACGTCGCGGCGAGCTCGCGCGCGAGGCGCA 214
 QY 342 GGGCGAGGCGGCGCTCCAGAAAGCCGAGAGGCGCAAAAGGCGCAAAAGCAGCAGCTGAG 401
 DB 215 GGAGCGCGCGGGGAGAAAGAGGCGAGGCGAGAAAGAGGCGCGCGCTGCTGTC 274
 QY 402 TCTGAGAAAGTGAAGGCTCAGATCGGCAACCGCACCTGCGCGGCTGTGACGCGCGC 461
 DB 275 GCTTGAAGAAAGTGAAGGCTGAAGTCCGGAACCGCACCTTCGCGCGCTGTGACGCGCGC 334
 QY 462 CATCGCGCGCGCGCTGTCGAGAGATTTCGTGCGCGCACCTGAGAGAGATCAGACGACCT 521
 DB 335 CATCGCGCGCGCGCTGTCGAGAGATTTCGTGCGCGCACCTGAGAGAGATCAGACGACCT 394
 QY 522 GATGTTGGGAGACTCCGCGCGGACCTCCATGCGCGGAGTTTTCGCTGATCATGCGAGC 581
 DB 395 CATGTTGGGAGACTCCGCGCGGACCTCCATGCGCGGAGTTTTCGCTGATCATGCGAGC 454
 QY 582 GGAAGGAGGAGCGCGGCTCTTCGCGGCAAGCGCGTCAAGCTGTCGCGCGCGCAAG 641
 DB 455 CGAGGCTGAGACCGGCTCTTCGCGGCAAGCGCGTCAAGCTGTCGCGCGCGCAAG 514
 QY 642 CAAGGCGCATC--GAGCACTTCACTTACGACAGCGCGCAAGAGTACTGACCCCGAGGCGC 699
 DB 515 CAAGGCGCATCAGAGAGATTTCACGACAGCGCGCAAGAGTACTGACCCCGAGGAGC 574
 QY 700 GCGGAGCGCAGGAGGTTCCCATCCGCGCGCTGTGCGGAGCGCTCGCGGAGTG 759
 DB 575 GCGGAGCGCTGCGCAAGATCCCATCCCGCTGCTGTCGCGGCGCGCTCGCGGTCGTC 634
 QY 760 GGTGCAACCTGTGCACTTCCATCCATGAGCTGTCGAAGACCGCTGCAACCTGA--GA 817
 DB 635 GCTTCAACCTGTGCACTTCCATCCATGAGCTGTCGAAGACCGCTGCAACCTGAAGAG 694
 QY 818 AGGACGTGACGACAACTCTCTCAAGCGCTTGTCAAGATCTGTGCGAGCGAGGCGCGG 877
 DB 695 AGGACGTGACGACAACTCTCTCAAGCGCTTGTCAAGATCTGTGCGAGCGAGGCGCGG 754
 QY 878 GGAAGCTGTACCGCGGCGCTGCGCGAGCGCTGATGCGCGCTGTGCGCTGACGCGGCGCA 937
 DB 755 GGAAGCTGTACCGCGGCGCTGCGCGAGCGCTGATGCGCGCTGTGCGCTGACGCGGCGCA 914
 QY 938 ACTTCTACGCTTACGAGAGCTGCGCGCTGTGTACCGCGCGCGCGCGCGCGCGCG 996
 DB 815 ACTTCTACGCTTACGAGAGCTGCGCGCTGTGTACCGCGCGCGCGCGCGCGCGCG 874
 QY 997 GTGGGCAAGTCCCGAGCGCTGATGCGGTCGCGCGGCGCGCGCTTACGAGCGCGC 1056
 DB 875 GTGGGCGCGCGCGCGCGCGCTGCTGCTGCGGTCGCGCGGCGCGCGCTTACGAGCGCGC 934
 QY 1057 AGCTTCCGCTGAGGTTGCGCGGAGAGAGATGAGTGGGCGCGCTGCGCGGAGGCGAG 1116
 DB 935 ACCTTCCGCTGAGGTTGCGCGGAGAGAGATGAGTGGGCGCGCTGCGCGGAGGCGAG 994
 QY 1117 GTGTACAAAGAGCTGTGACGCGCATGTACTGATCTCTGAGAGAGAGGCGACCGCGGG 1176

DB 995 GTGTACCGCGCGCTGCGCGCGAGCGCATCAAGCTCATAGCCCGCGCGCATCTCTTC 1054
 QY 1177 CTTCACCGCGCGCTGCGCGCGAGCGCATCAAGCTCATAGCCCGCGCGCATCTCTTC 1236
 DB 1055 CTTCACCGCGCGCTGCGCGCGAGCGCATCAAGCTCATAGCCCGCGCGCATCTCTTC 1114
 QY 1237 ATGTGCTACGAGGCGCTGCAAGAGTACTTGTGACGAGAAAG 1279
 DB 1115 ATGTGCTACGAGGCGCTGCAAGAGTACTTGTGACGAGAGAGG 1157

RESULT 3

ADJ41898 standard; cDNA; 698 BP.

ADJ41898; 06-MAY-2004 (first entry)

Plant cDNA #2898.

KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
 KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
 KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
 KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
 KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
 KW antifungal.

OS Eukaryota.

PN US2004016025-A1.

PD 22-JAN-2004.

PF 26-SEP-2002; 2002US-00260238.

PR 26-SEP-2001; 2001US-0325277P.

PR 26-SEP-2001; 2001US-0325448P.

PR 04-APR-2002; 2002US-0370620P.

PA (BUDM/) BUDMORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S. P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZEBROOK J.
 PA (GOLF/) GOLF S. A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICHE D.
 PA (ZHUT/) ZHU T.

PI Budworth P., Moughamer T., Briggs S.P., Cooper B., Glazebrook J;
 PI Goff S.A., Katagiri F., Kreps J., Provart N., Riche D., Zhu T;
 XX WPI; 2004-190374/18.

PT New rice promoter, useful for manipulating crop plants to alter or
 PT improve phenotypic characteristics, e.g. produce large quantities of oil
 PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
 PT or high nutritional value.

PS Example 13; SEQ ID NO 2898; 230bp; English.

XX The invention relates to plant nucleotide sequences that direct seed-,
 CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
 CC or constitutive transcription of an operatively linked nucleic acid
 CC segment. The invention also relates to a method for augmenting a plant
 CC genome and a method of identifying a gene, where its expression is
 CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
 CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
 CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

Db 60 CAACGTGCCAGCCTCTGATC-GGTCCGCGCGCGGCCCATAGCAGCACCCGCACGTT 118
 Qy 1062 CCCGCTGAGGTGGCGCGGAGAGATGACAGTGGGCGCGTGGGGGAGGAGAGTGTGA 1121
 Db 119 CCGCTGGAGGTGGCGCGGAGAGATGACAGTGGGCGCGTGGGGGAGGAGTGTGA 178
 Qy 1122 CAAGAACGTGTGACGCGCATGTACTGTACCTCTGAGAAAGAGAGGAGCGCGGGCTCTA 1181
 Db 179 CAAGAACGTGTGACGCGCATGTACTGTACCTCTGAGAAAGAGAGGAGCGCGGGATCTTA 238
 Qy 1182 CCGCGGCTCGCGCGCCAGCTGATCAAGCTCATGCCCGCGCGGAGTCTCTTCATGTG 1241
 Db 239 CCGCGGCTCGCGCGCCAGCTGATCAAGCTCATGCCCGCGCGGAGTCTCTTCATGTG 298
 Qy 1242 CTACGAGGCTCGAAGAAATTAATTTCTGACGAGAAAGAGAGGAGCGCGGGCGCGAGCC 1301
 Db 299 CTACGAGGCTCGAAGAAATTAATTTCTGACGAGAAAGAGAGGAGCGCGGGCGCGAGCC 346
 Qy 1302 CCAGAGAGAGACGAGACCGGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1361
 Db 347 CCAGAGAGAGACGAGACCGGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 406
 Qy 1362 TGATCGGCGCATGAACTAGATGAAGCATTTATGTGACCGTCAAAATCAGAAAGAAATGCGT 1421
 Db 407 TGCTCGCCCATGAAACCGATGAAGCATTTATGTGACCGTCAAAATCAGAAAGAAATGCGT 466
 Qy 1422 GATTTAAATTTTGAAGGTAGAGAGCTTATGGGATTTGAATCTTAAGCTGGAAGTGGCG 1481
 Db 467 GATTTGAAA-TTTTGAAGGTAGAGAGCTTATGGGATTTGAATCTTAAGCTGGAAGTGGCG 525
 Qy 1482 CTTAGAAGTTGAATTTGTTTTGTTCAGGAGAACATGCTCGTTGATGATGCGCGTGA 1541
 Db 526 CTTAGAAGTTGAATTTGTTTTGTTCAGGAGAACATGCTCGTTGATGATGCGCGAAGT 585
 Qy 1542 TGATTTATGCACTTTCTGTATCAATTCATTAAGAGAAAGTCCACTTTTGAGCC 1598
 Db 586 TGATTTATGCACTTTCTGTG-ATCAATTCATTAAGAGAAAGTCCACTTTTGAGCC 640

RESULT 5
 ADJ42969
 ID ADJ42969 standard; cDNA; 661 BP.

AC ADJ42969;

DT 06-MAY-2004 (first entry)

XX Plant cDNA #3969.

XX Plant; gene; ss; transcription; plant genome augmentation; cereal;
 KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
 KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
 KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
 KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
 KW antifungal.

XX Eukaryota.

XX US2004016025-A1.

XX 22-JAN-2004.

XX 26-SEP-2002; 2002US-00260238.

XX 26-SEP-2001; 2001US-0325277P.

XX 26-SEP-2001; 2001US-0325448P.

XX 04-APR-2002; 2002US-0370620P.

XX (BUDWORTH P.
 PA (MOUGHAMER T.
 PA (BRIGGS S P.
 PA (COOPER B.
 PA (GLAZZ/) GLAZEBROOK J.

PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICHE D.
 PA (ZHUT/) ZHU T.
 PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
 PI Goff SA, Katagiri F, Kreps J, Provart N, Riche D, Zhu T;
 XX WPI; 2004-190374/18.
 DR
 PT New rice promoter, useful for manipulating crop plants to alter or
 PT improve phenotypic characteristics, e.g. produce large quantities of oil
 PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
 PT or high nutritional value.
 PS Example 13; SEQ ID NO 3969; 230bp; English.
 XX
 CC The invention relates to plant nucleotide sequences that direct seed-,
 CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
 CC or constitutive transcription of an operatively linked nucleic acid
 CC segment. The invention also relates to a method for augmenting a plant
 CC genome and a method of identifying a gene, where its expression is
 CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
 CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
 CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
 CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
 CC encode are useful for manipulating crop plants to alter or improve
 CC phenotypic characteristics, to produce large quantities of oil or
 CC proteins, to incur resistance to insecticides, viruses or fungi, and to
 CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
 CC have a high nutritional value with reduced apical dominance or dwarfism,
 CC early flowering or altered metabolic pathways. This sequence represents a
 CC plant nucleic acid of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification but was obtained in
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 661 BP; 160 A; 177 C; 202 G; 122 T; 0 U; 0 Other;
 Query Match 31.4%; Score 511; DB 12; Length 661;
 Best Local Similarity 91.7%; Pred. No. 2,3e-88;
 Matches 578; Conservative 0; Mismatches 34; Indels 18; Gaps 3;
 Qy 1000 GGCACGTCGCCAGCGTGTGATCGGGTCGGCGCGGCCCATAGCCAGCAGCGCACG 1059
 Db 35 GGCACGTCGCCAGCGTGTGATCGGGTCGGCGCGGCCCATAGCCAGCAGCGCACG 92
 Qy 1060 TTCCCGCTGGAAGTGGCGCGGAGAGAGATGAGTGGGCGCGTGGCGGGAGGAGG 1119
 Db 93 TTCCCGCTGGAAGTGGCGCGGAGAGAGATGAGTGGGCGCGTGGCGGGAGGAGG 152
 Qy 1120 TACAAAGACGTCTGCAACCGCATGTACTCATCTCTGAGAAAGAGAGGAGCGCGGGCTC 1179
 Db 153 TACAAAGACGTCTGCAACCGCATGTACTCATCTCTGAGAAAGAGAGGAGCGCGGGCTC 212
 Qy 1180 TACCGGAGGCTCGGCCCGACGTGATCAAGCTCATGCCCGCGCGGCATCTTTCATG 1239
 Db 213 TACCGGAGGCTCGGCCCGACGTGATCAAGCTCATGCCCGCGCGGCATCTTTCATG 272
 Qy 1240 TGCTACGAGGCTTGCAAGAAATTAATTTCTGACGAGAAAGAGAGAGCGCGCGCGAG 1299
 Db 273 TGCTACGAGGCTTGCAAGAAATTAATTTCTGACGAGAAAGAGAGAGCGCGCGCGAG 320
 Qy 1300 CCCAAGAGAGAGACGAGACCGGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1359
 Db 321 CCCAAGAGAGAGACGAGACCGGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 380
 Qy 1360 GGTGATCGGCATGAACTAGATGAAC---ATTATGTGACCGTCAAAATCAGAAAGAA 1415
 Db 381 GGTGATCGGCATGAACTAGATGAAC---ATTATGTGACCGTCAAAATCAGAAAGAA 440
 Qy 1416 ATGCGTGAATTTTGAAGTGTAGAGGCTTATGGGATTTGAATCTTAAGCTGGAAG 1475

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Db      441 ATGCGTGAATTTGAATTTTGAAGTGAAGCCAGTGAATGAATCCTAAGCTGAGAG 500
QY      1476 TGGGCGCTTGAAGTTGAATTTGTTTGTTCAGGGAAACATGCTCCGTTTCAGTAATGCC 1535
Db      501 TGGGCGCTTGAAGTTGAATTTGTTTGTTCAGGGAAACATGCTCCGTTTCAGTAATGTC 560
QY      1536 GTGCAATGATTTATGAGCACTTCTGTATCAATTCATTAAGAAAGTCCAATTG 1595
Db      561 GTGCAATGATTTATGAGCACTTCTGTATCAATTCATTAAGAAAGTCCCTTTGG 620
QY      1596 ACCTTCAAAAAAATTTTCAAAAAAATTTTCAAAAAAATTTTCAAAAAAATTTTCA 1625
Db      621 ACCTTCAAACTTTGCCCCCAAAAAAATTTTCAAAAAAATTTTCAAAAAAATTTTCA 650

RESULT 6
ADJ42974
ID      ADJ42974 standard; cDNA; 1056 BP.
XX
XX      ADJ42974;
AC
XX      06-MAY-2004 (first entry)
DT
XX
XX      Plant cDNA #3974.
DE
XX
XX      Plant; gene; ss; transcription; plant genome augmentation; cereal;
KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KM stress tolerance; salt tolerance; drought tolerance;
KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KM antifungal.
XX
XX      Eukaryota.
OS
XX
XX      US2004016025-A1.
PN
XX
XX      22-JAN-2004.
PD
XX
XX      26-SEP-2002; 2002US-00260238.
PF
XX
XX      26-SEP-2001; 2001US-0325277P.
PR      26-SEP-2001; 2001US-0325448P.
PR      04-APR-2002; 2002US-0370620P.
XX
XX      (BUDW/) BUDWORTH P.
PA (MOUN/) MOUNHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREBS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHKE D.
PA (ZHUT/) ZHU T.
XX
XX      Budworth P, Mounhamer T, Briggs SP, Cooper B, Glazebrook J;
PI Golf SA, Katagiri F, Krebs J, Provart N, Riche D, Zhu T;
XX
XX      WPI; 2004-190374/18.
DR
XX
XX      New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.
XX
XX      Example 13; SEQ ID NO 3974; 230pp; English.
XX
XX      The invention relates to plant nucleotide sequences that direct seed-,
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant

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CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/Sequence.html.
XX
XX      Sequence 1056 BP; 264 A; 256 C; 288 G; 248 T; 0 U; 0 Other;

Query Match      27.1%; Score 440.4; DB 12; Length 1056;
Best Local Similarity 71.0%; Pred. No. 8.1e-75;
Matches 598; Conservative 0; Mismatches 241; Indels 3; Gaps 1;

QY      494 CGCCACTGAGAGCATCAGACGACACTGATGATGGAGAGCTTCGCGGCACTCCATG 553
Db      1 CGCCGTTGAGAGCAATTTAGACACACTGATGGTTGGAGCATGG---GGATTCAATGA 57
QY      554 CCGGGGTTTTCCGGTGATCATCGGACGAGGGGTGGCCCGGCTCTTCCGCGCAACG 613
Db      58 CAGAGGTTGTTTCAGACAAATATGAAAGTGGAGGGCTGAGACAGGGCTGTTCCGAGGAAC 117
QY      614 CGCTCAACGTCCTCCGCGCTCCGCCCAAGAGCCCATTCAGACCTCACTTACGACACGG 673
Db      118 TTGTAAATGTTATCCGTGTGCTCCAGCAAGCGATGAGCTATTTGCTTTGATATACAG 177
QY      674 CGAAGAATGATCTGATCCCGGAGCGGCGAGCCAGCCAAAGTCCCATCCACGCGCG 723
Db      178 CCAAAAATTTCTGACTCCAAAGGCTGATGAGTCTCTTAAGACCCCTTCCCTCAATCAC 237
QY      734 TCGTGCCTGGAGGCGCTCGCCGAGTGGCGCTCAACCTGTGACCTTATCCATGAGCTCG 793
Db      238 TTGTGCGGGGGGACATTGACAGTGTGACGCTCAACACTGACATATCTCTGGAAC 297
QY      794 TCAAGACCGCTCTCACATCGAAGAAAGAGCTGTACGACAACTCTCCACGCGGTGTCA 853
Db      298 TCAAGACCGCTCTGACTATAGAGAAAGAGCTATATGACAACTTCTTCATTCGCTGCTCA 357
QY      854 AGATCGTGCGGAGCGAAGAGCGCGGGAGAGCTGTACCGCGGCTGCGCCGAGCCTGATCG 913
Db      358 AGATTGTACAGAGAGAGAGGCGCTTCGAGGCTTTTACCGTGTCTGACACGAGCTGATAG 417
QY      914 GCGTGTGCGGTAAGCGGCGGCGCACTTCTAGCGCTTACGAGAGCTGCGCGGCTGATCC 973
Db      418 GAGTGGTGCAATATGCGCGGACCACTATACGCTTACGACACCTGAGGAAAGCTGTACA 477
QY      974 GCCCGCGGTGGGGAAGAGAGAGTGGGCACTCCCGAGAGCTGTGATGGGGTCCGCGG 1033
Db      478 GGAAGACATTCAGAGAGAGAGATGAGCAACTTGCACACCTCTGTATGCTTGGCGCG 537
QY      1034 CGGGCGCATATGACGAGAGCGGACGCTTCCCGCTGAGAGTGGGCGGGAAGCAGATGAGG 1093
Db      538 CGGGCGCATCTGAGAGACCGCACTTCCCTCTCGAAGTATGCTCCGACAGCATGAGG 597
QY      1094 TGGGCGCGCTGAGCGGAGGAGCAGGTGTACAAAGAGCTGTGACGCCCATGATGATCC 1153
Db      598 CAGGGGCGGTGGGCGGAGGCAAGTGTACAAAGAGCTGTGACGCCCTACTGATGATGA 657
QY      1154 TCAGAAAGAGGAGCGCGCGGCTTACCGCGGCTCGGCCCGCAGTGTGATGATGATGTA 1213
Db      658 TGAGAAAGAGGAGATCGCGGCTGTGTACAGAGGCGCTTGGGCCCATGATGATGATGTA 717
QY      1214 TGGCGCGCGCGGCGATCTCTTATGATGCTGACGAGGCGTTCAGAAAGATCTTGTGACG 1273
Db      718 TGGCGCGCGGCGGATCTCTTATGATGCTGACGAGGCGTTCAGAAAGATCTTGTGACG 777

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QY	1274	AGAAAGAGACGGCGCGCCCGCCGAGCCCGCCAGAGAGACGAGACCGGACAGGAGAG	1333
DB	778	CCGAGAGATTAGACCGAAGTGGCGCCACCGGTGTCTGGGTCTTAAAGAAAGAGCGCGAGAG	837
QY	1334	GA 1335	
DB	838	GA 839	
RESULT 7			
ID	AAZ20025	standard: cDNA, 1267 BP.	
AC	AAZ20025;		
XX			
XX	21-DEC-1999	(first entry)	
XX			
DE	Wheat brittle-1 partial cDNA.		
XX			
KM	Brittle-1; wheat; carbohydrate; starch; transgenic plant; ss.		
XX			
OS	Triticum aestivum.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	2..871	
FT		/*tag= a	
FT		/partial	
XX			
PN	MO9949047-A2.		
XX			
PD	30-SEP-1999.		
XX			
XX	22-MAR-1999;	99WO-US006583.	
XX			
PR	26-MAR-1998;	98US-0079420P.	
XX			
PA	(DUPO) DU PONT DE NEMOURS & CO E. I.		
XX			
PI	Allen SM, Hitz WD, Lightner JE, Rafalski JA;		
XX			
DR	WPI; 1999-591098/50.		
DR	P-PSDB; AAY31936.		
XX			
PT	Novel genes useful in studies of carbohydrate metabolism and function in		
PS	plants.		
PS	Claim 7; Page 42; 42pp; English.		
XX			
CC	This nucleotide sequence represents a portion of the cDNA insert in clone		
CC	wrein, pK0049, ei encoding a portion (see AAY31936) of wheat brittle-1, a		
CC	plasticidic membrane transporter involved in the transport of ADP-glucose		
CC	from the cytosol to the plastid where it is used for starch biosynthesis.		
CC	The clone was isolated from a wheat root cDNA library. The invention		
CC	relates to isolated nucleic acid fragments (see AAZ20012-25) encoding		
CC	plant carbohydrate biosynthetic enzymes (see AAY31923-36) selected from		
CC	1,3-beta-D-glucan synthase and brittle-1. It also relates to the		
CC	construction of a chimeric gene encoding all or a portion of a		
CC	carbohydrate biosynthetic enzyme, in sense or antisense orientation,		
CC	where expression of the chimeric gene results in altered levels of		
CC	carbohydrate biosynthetic enzyme in a transformed host cell. The		
CC	availability of nucleic acids encoding these enzymes will facilitate		
CC	studies of carbohydrate metabolism and function in plants, provide		
CC	genetic tools for the manipulation of these pathways, and provide a means		
CC	to control starch and 1,3-beta-D-glucan biosynthesis in plant cells		
XX			
SO	Sequence 1267 BP; 351 A; 268 C; 317 G; 331 T; 0 U; 0 Other;		
Query Match	24.6%;	Score 400.2;	DB 2; Length 1267;
Best Local Similarity	66.8%;	Pred. No. 4,1e-67;	
Matches 586;	Conservative 0;	Mismatches 288;	Indels 3; Gaps 1;
QY	415	AGGTCGAAGATCGGCACCCGACCTCGCGCGCTGTGTCAGCGGCGCCATCGCCGCGCC	474

Db	2	AAGATTAAAGTTGGGAATTCACACCTCAAGAGGCTCATCACTGGGGGGATTGCAGAGCA	61
Oy	475	GTTTCGAGGACCTTTTCGTGGCCGCACTGGAGACGATCAAGACGCACTGATGGTGGGAGC	534
Db	62	GTTTCAGGACAGTTGTGGGGCTTTGGAGACGATTAGACACTTTGATGGTGGCAGC	121
Oy	535	TCCGGCCGCACTCAATGGCCGGGGTTTCCGATGATCATGCCGACGGAGGGTGGCC	594
Db	122	AATGGGAATTCATCTACGAGAGGTGTTGAC--TCATCATGAAGAAATGAAGATGACT	178
Oy	595	GGCCCTTTCGGGGGCAACGCCGTCAAGTCTCCGGGTCCGGGCCAAGCCATCGAG	654
Db	179	GGGTGTTCGGGGCAATTGGTTAAATGCACTTGAGTCCGCCAGACAAAGCAATCGAG	238
Oy	655	CACCTCACTTACGACAGCGCGAAGAAATGACTGACCCCGGAGCGCGCGACCGCAAG	714
Db	239	CTTTTGTGCTTTGATACGCTAAGATTTCTTAACCCCAATCTGGGGAAGACAGAG	298
Oy	715	GTCGCCATCCCCACGCGCTGTGCGCCGAGACGCTGCCCGAGTGGCGTCAACCTGTGC	774
Db	299	ATCCCAATCCCTCCTTCACTAGTGGCAGAGACTTTTCTGGTGTCAACTACTGTGT	358
Oy	775	ACCAATCCCAATGAGAGCTGTCAACACCCGTCTCACTCAAGAAAGACGTGTACGAAC	834
Db	359	ACATAACCTCTGGAACTAATTAAACCTCGATTAAACATAAGAAAGGTGTATGATTAC	418
Oy	835	CTCCTCCACGCGTTCGTCAAGATGTCGTCCGACGACGAGCCCGGGGAGCTGTACCGCGG	894
Db	419	TTCTCTCAATGATTTGTGAAATTTGTCGTGTAGAAAGGCCCTGTGAGCTGTATAGGCC	478
Oy	895	CTGGCGCCGAGCCTGATCGCGGTGTGCGGTGCGGTGCGGCGCACTTCTACGCTACGAG	954
Db	479	TTAACCCCAAGTAAATCGAGGTGTGTCATATGACAGCAACCAACTACTTCGGGTATGAC	538
Oy	955	ACGCTGGCGGCGGTGTACCGCGCGCGCTCGGGGAAAGAGGTGGCAACGTCCGACG	1014
Db	539	ACCTTTAAGAAAGGTGTCAAGAAATATTTCAAGCAATGAATTCGGCAACGTTCCAAAC	598
Oy	1015	CTGCTGATCGGGGTCCGGCGCGGCGCCATATGACGACGCGCACTTCCCGCTGAGAGTG	1074
Db	599	CTGCTCATTTGGGTGTGTCGACGAGCCATCTCAAGCACTGCCACATTTCTTTCGAGGTT	658
Oy	1075	GCGCGGAAGACAGATGACGAGTGGCGCGCGGTGGGCGGAGGACGAGTGTACAAAGACGTG	1134
Db	659	GCTGCAAGACACATGCAAGTCCGAGCTGTTGGCGCGGGAAGGTATACAAAGACATGCTT	718
Oy	1135	CAGCCCATATACAGTCACTCTCGAAGAGAGGACCGCCGGGCTTACCGCGGGCTCGGC	1194
Db	719	CACCTCTCTGACCATTTCTCGAAGAGAGAGGGGTTGGGGGCTCTTACAAAGACATGGGG	778
Oy	1195	CCGAGCTGATCAAGCTCATGCCCCGCGCGGCATCTCTTCAATGTGCTACGAGGCGCTGC	1254
Db	779	CTTATTTGCAATGAAGCTGTGTGCTGCTGCTGTGGGATTTCTTTTATGTGTCTAGAACTTGC	838
Oy	1255	AAGAAGATACTGTGTGACGAGAAAGAAAGACGCGCGCG	1291
Db	839	AAGAAGATACTGATTTGAGAAAGAAAGAAATGAAGCG	875
RESULT 8			
AAD57636			
AAD57636 standard; DNA; 1140 BP.			
XX	AAD57636;		
XX	AC		
XX	AD57636 (first entry)		
DE	Rice grain quality and nutritional composition gene, BTL.		
XX	Rice; abiotic stress tolerance; pathogen resistance; disease resistance;		
KM	grain quality; nutritional content; plant yield; BTL; plant; gene; db.		
XX	Oryza sativa.		
3S			

Db	299	GCAGCAACTACTATGCTTACGACACCTCTGAGAAAGCTCTACAGAAAGACATTCAAGCAG	358
Qy	991	GAGAGAGTGGGCAACGTCCTCCGACGCTGCTGATTCGGGATCCGGCGGGCCCATAGCCAGC	1050
Db	359	GAGAGGATACAGCAACATTGCAAACTCTCCTGATTCGGTTCCGCGGGGGCCATCTCGAGC	418
Qy	1051	ACGGCCACGTTTCCCGCTGGAAGTGGCCGCGAAGCATATGCAGTGGGGCCCTGTGGCGGG	1110
Db	419	ACCGCCACCTTCCCTCTCGAAGTAGCTTCGCAAGGAGATGCAGGGCTGGGGCCGTGGCGGT	478
Qy	1111	AGGCAAGGTGTCAAGAAAGTCTGCAAGCCATGTACTGTGCATCTCTCGAAGAGAGGGCACC	1170
Db	479	AGGCAAGGTCTCAAGAAACGTGTTCATCTCTCTACTGTGCATTAATGAGAAAGAGGATC	538
Qy	1171	GCCGGGCTCTACCCGGGGCTCGGCCCCAGCTGCATCAAGCTCATGCCCGCCCGGAGTC	1230
Db	539	GCGGCGCTGTACAAAGGGGCTTGGGCTGTAGCTGCATCAAGCTCATGTCCCGCGGGGATC	598
Qy	1231	TCCTTCATGTGTCTACGAGGCGCTGCAGAAGATTACTTGTGACGAGAAAGAAAGACGGCGGC	1290
Db	599	TCGTTTCATGTGCTACGAGGCGCTGCAGAAGATTACTGTGCAAGCCGAGAGTAAACGAA	658
Qy	1291	GC 1292	
Db	659	GC 660	
RESULT 11			
AAAC49806			
ID	AAAC49806	standard; DNA; 1331 BP.	
XX	AC	AAAC49806;	
XX	DT	18-OCT-2000 (first entry)	
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 62505.		
XX			
KW	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway; metabolic pathway;		
KW	promoter; termination sequence; 5S.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-00301439.		
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Db      1127  ACAAGGCGCTTGACCGAGTGTGAAGTTGTTCCCTGCTGGAATCTCCTTCATGT 1186
Qy      1241  GCTACGAGCGCTGGAAGAGTACTGTTCGACGAGGAAGAGAG 1285
Db      1187  GTTATGAGCTTGCAAGAGTACTCATTCGAGAACCAAGAG 1231

RESULT 12
AAC35455
ID      AAC35455 standard; DNA, 1334 BP.
XX
AC      AAC35455;
XX
DT      17-OCT-2000 (first entry)
XX
DE      Arabidopsis thaliana DNA fragment SEQ ID NO: 10250.
XX
KW      Hybridisation assay; genetic mapping; gene expression control;
KW      protein identification; signal transduction pathway; metabolic pathway;
KW      promoter; termination sequence; ss.
XX
OS      Arabidopsis thaliana.
XX
PN      EP1033405-A2.
XX
PD      06-SEP-2000.
XX
PF      25-FEB-2000; 2000EP-00301439.
XX
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PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
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PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
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PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 22.0%; Score 357.8; DB 3; Length 1334;

Best Local Similarity 61.9%; Pred. No. 5.4e-59;

Matches 585; Conservative 0; Mismatches 357; Indels 3; Gaps 1;

QY 341 CCGGCGAGCGCGGCGTCCAGAAAGCCAGAGCGGCAAAAAGCCCAAAAAGCAGCGCTGA 400
DB 291 CCGGAAAGAGAGAGAGAGAAAGTAAATGCGAGAAAGAGAGAGAGAGAGAGAG 350

QY 401 GTCTGAGAGAGGTGAGGGTCAAGATCGGCAACCCGCACTCGCGGCTGTCTAGCGGCG 460
DB 351 GTGGGTGACACTGAAAGATTAAATCGTAATCTTTCGTTGCGGCGCTATTAAAGCGAG 410
QY 461 CCATGCGCGCGCGCGCTGTGTGAGAGACTTTGTGTGCGGCACTGAGAGATCAAGAGCCACC 520
DB 411 CAGTAGCTGAGACGGGTGTGAGAACGGTGTGTGCGCGCTTGGAGAGAAATCAGAGCCATC 470
QY 521 TGATGTGGGGAGCTCCGCGCGCGGCACTCCATGCGCGGGGTTTTCCGCTGATCATCGGAG 580
DB 471 TAAATGTGGAGG---TGAGAGAACTCCAGCACTGAAAGTTCACGTATATCATATAGC 527
QY 581 CCGAGGGGTGCGCCGCGCTCTTCCGCGGCAACCGCTCAACGTCCTCCGCTCGCGCCA 640
DB 528 ATGAAAGTTTGAAGCTGTCTCTTCAAGGGGCAATTTGTGTAATGATCATGTTTGAACCTG 587
QY 641 GCAAGGCCATCGAGCACTTCACTTACAGACGCGGAGAGAGTAACTGACCCGAGGCGCG 700
DB 588 CTCGAGCCGTCGAGCTTTTGTATTCGAGACCGTAAACAAAGAAATGTGCGCGCCACATG 647
QY 701 GCGAGCCAGCGAAGGTCCCATCCCAAGCGCGCTGTGCGGAGCGCTCGCGGAGTGG 760
DB 648 GACAAAGATCGAAAAATCCCAATTCAGCTTCTTTACTGCTGCTGTGTGAGTGA 707
QY 761 CGTCAACCTGTGACACTATCCATGAGCTGTCAAGACCCGCTCACCATCGAGAGAG 820
DB 708 GCCAGACACTTGTGACATACCTCTTGAACCTGACAGCTGCTTCAATTCAGAGAG 767
QY 821 ACGTGTACGACAACTCTTCCACGCGTGTGTCAAGATCTGTGCGGACGAGGCGCGGAG 880
DB 768 GTGTTTACAAAGGATTTTGTGATGCGTTTCTCAAAATCAATGACGAGAGAGACCCACAG 827
QY 881 AGCTGTACCGCGGGGTGTGCGCGGACCTGTATGCGGCTGTGCGGAGCGGCGCAACT 940
DB 828 AACTCTTACAGGGGTCTTGTCTTCTTACCTTATGTGAGTGTTCATACGAGCTTCAAAAT 887
QY 941 TCTACGCTTACGAGACGCTGCGCGGCTGTACCGGCGCGGCTGTGCGGAGAGAGAGTGG 1000
DB 888 ACTTGTGATATATATCTTGTGAGAAAAAGCATACCGAGTTTTCMAAGCAGAGAAAGATTG 947
QY 1001 GCAACGTCCCGACGCTGTGATCGGGTCCGCGGCGGCGCCATAGCCAGACGCGCCACGT 1060
DB 948 GAAACATTGAGACTCTTTTGTATGAGTTCTTGTAGCAGGTGCACTATCGAGCACTGCAACT 1007
QY 1061 TCCCGCTGAGGTGTGCGGAGAGAGATGACAGTGTGGCGCGGAGAGGAGGCTGT 1120
DB 1008 TCCCTCTTGAAGTGTGCGGAGAGCATATGACGTGTGGAGCTGTGTGCGGAGAGGTTGT 1067
QY 1121 ACAAGAACGTGTGACGCGCATGTACTGATCTGTGAGAGAGAGGAGCAACGCGCGGCTCT 1180
DB 1068 ACAAGAACATGTTGACAGCTCTGTGTACCATATCTTGAAGCATAGAGTATTTCTCGTTGT 1127
QY 1181 ACCGCGGCTCGGCGCCAGCTGACATCAAGCTCATGCGCGCGCGCATCTCTTCATGT 1240
DB 1128 ACAAGGGCTTGGACGAGGTTGCTTGAAGTTGCTGTCTGTCTGTGAAATCTCTTCATGT 1187
QY 1241 GCTACGAGGCTTGAAGAGATATCTTGTGACGAGAGAGAGACG 1285
DB 1188 GTTATGAGACTTGAAGAGATATCATCATGAGAGAACCAAGAG 1232

RESULT 13

AD042973 standard; cDNA; 653 BP.

AD042973;

AD042973; (first entry)

06-MAY-2004

Plant CDNA #3973.

Plant; gene; ss; transcription; plant genome augmentation; cereal;
soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;

KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KM antifungal.
XX
OS Eukaryota.
PN US2004016025-A1.
XX
PD 22-JAN-2004.
XX
PF 26-SEP-2002; 2002US-00260238.
XX
PR 26-SEP-2001; 2001US-0325277P.
PR 26-SEP-2001; 2001US-0325448P.
PR 04-APR-2002; 2002US-0370620P.
XX
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B. B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREBS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHKE D.
PA (ZHUT/) ZHU T.
XX
PI Budworth P., Moughamer T., Briggs SP, Cooper B, Glazebrook J,
PI Goff SA, Katagiri F, Krebs J, Provart N, Riche D, Zhu T;
XX
DR WPI; 2004-190374/18.
XX
XX
PT New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.
XX
PS Example 13; SEQ ID NO 3973; 230bp; English.
XX
CC The invention relates to plant nucleotide sequences that direct seed-,
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 653 BP; 163 A; 160 C; 190 G; 140 T; 0 U; 0 Other;
XX
Query Match 15.8%; Score 256.8; DB 12; Length 653;
Best Local Similarity 74.1%; Pred. No. 1.1e-39;
Matches 338; Conservative 0; Mismatches 117; Indels 1; Gaps 1;
QY 834 CCTCTCTCAGCGCTTGCACGATCGTCCGCGAGAGAGCCCGGGAGCTGACCGCGG 893
DB 1 CTTTCTCCATTGCTCTCGTCAAGATTGAACGAGAGAGAGCCCTTCGAGGCTTTCCGTTG 60
QY 894 GCTGGCCGCGAGCTGATC-GGCGTGGTCCGCTGACGGCGGCCCACTTACCGCTTACG 952
DB 61 TCTGACCGCGAGCTGATGAGGAGTGGTCCATACGCGCGGACCACTACATATCCCTTACG 120

QY 953 AGACGTGCGCGGCGTGTACCCGCCGCGTCCGGGAAAGAGAGTGGCAACGTCCCGA 1012
DB 121 ACACCTTGAGGAAGCTCTACAGAAACATTTCAAGAGAGAGAGATCAGCAACTTGCA 180
QY 1013 CGCTGTGATTCGGGTCCGCGCGCGCATACCGACACGCGACGTTCCGCTGAGG 1072
DB 181 CCTCTGTATTTGGTTCGGCGCGCGGCATCTCGACATCGCACCTTCCCTCTGAAAG 240
QY 1073 TGGCGCGGAAAGAGATGCGAGTGGCGCGGTGGCGGGAGGAGCGGTCAAGACGTG 1132
DB 241 TAGCTCGAAGCAAAAGTCAAGGCTGGGCGGTGGTGAAGGAGGTCTACAAAGACTGT 300
QY 1133 TGACCCCATGTACTGCTCATCTCGAAGAGAGGCAACCGCGGCTTACCGCGGCTCG 1192
DB 301 TCCATGCCCTCTACTCATTAATGAGAAAGAGAGATGGCGGCTGTACAAAGGGCTCG 360
QY 1193 GCCCAGCTGATCAAGCTCATGCCCGCGCGCATCTCTCATGTGCTACGAGGCT 1252
DB 361 GGCCAGCTGATCAAGCTCATGCCCGCGCGGATCTCTCATGTGCTACGAGGCT 420
QY 1253 GCAGGAAGATCTTGTGCAAGAGAAAGAGACGGCG 1288
DB 421 GCAGGAAGATCTTGTGCAAGCGGAGAGTGAAGCG 456
RESULT 14
AAC49805
ID AAC49805 standard; DNA; 829 BP.
XX
AC AAC49805;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 62501.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic pathway;
KM promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
XX EPI033405-A2.
PN
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
PF
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0128234P.
PR 06-APR-1999; 99US-0128714P.
PR 08-APR-1999; 99US-0129845P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
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PR 11-MAY-1999; 99US-0134256P.
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PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
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PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
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PR 20-JUL-1999; 99US-0144632P.
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PR 17-AUG-1999; 99US-0148175P.
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PR 26-AUG-1999; 99US-0150884P.
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PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.

PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161931P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 15.6%; Score 253.8; DB 3; Length 829;
Best Local Similarity 62.6%; Pred. No. 4.1e-39;
Matches 396; Conservative 0; Mismatches 237; Indels 0; Gaps 0;

QY 653 AGCACTTCACTTACGACACGCGGAGAGTACTGACCCCGAGCGCGGACGACCA 712
Db 5 AGCTTTTGTATTGAGACCGTAAACAAGAAATTGTGCGCCGACATGAGACAAGATCGA 64
QY 713 AGGTCCCATCCCAACGCGCGCTGTCGCGGAGCGCTGCGGAGTGCGCTCAACCTGT 772
Db 65 AAATCCCAATTCCAGCTTCTTACTGCGTGTGCTGTGCTGTGAGATTAGCCAGACACTCT 124
QY 773 GCACCTATCCCATGAGAGTCTGCAAGACCCGCTTCACATGAGAGAAAGCTGACACA 832
Db 125 TGACATACCCCTCTTGAAGTACTGACAGCTGCTTACATTCAGAGAGGTGTTTCAAG 184
QY 833 ACCTCTCCACGCGCTTGTGTCAGATCGTCGCGACGAGCGCGGAGGCTGTACCGCG 892
Db 185 GGATTTTGTATGCTTTCTCAAAATCATACGCGAGAGAAAGCCACAGAACTCTACAGGG 244
QY 893 GGTGGCGCGGAGCGCTGATCGCGCTGTGTCGCTGACGCGCGGCGCACTTCTACGCTACG 952
Db 245 GCTTGTCTCTAGCCTTATTGAGATTGTTTCATACGCGAGCTACAAATTACTTTCATATG 304
QY 953 AGAGCTGCGCGGAGGTGATACCGCGCGCGCTGTGCGGAGAGAGAGAGTGGGCACTCCCGA 1012
Db 305 ATTCTTTTGAAGAAAGCATACCGAGTTTTCAAAGCAGAGAAAGATTGGAACATTGAGA 364
QY 1013 CGTGTGATCGGCTCGCGCGCGCGCATAGCAGACGCGCCATCTCCCGTGGAGG 1072
Db 365 CTCCTTTGATAGTTCCTTTAGCAGGTGACATATGAGACATCTTCCCTTTTAAAG 424
QY 1073 TGGCGCGGAGACAGATGAGGTGGCGCGCTGTGGCGGAGGACAGTGTACAAAGACGTGC 1132
Db 425 TGGCCCGGAGCATATGAGGTGGAGCTGTTACGCGAGGCTTGTGACAAAGCAATGT 484
QY 1133 TGCACGCGCATGTATGATCTCTCGAAGAGAGGACACCGCGGCTCTACCGCGGCTCG 1192
Db 485 TGCACGCTCTGTGTACCATATCTTGAGCATGAAAGGTATTCTCGTGTGTACAAAGGCTTG 544
QY 1193 GCCCAGCTGATCAAGGTCAATGCGCGCGCGCATCTCCTTATGATGCTACGAGGCT 1252
Db 545 GACCGAGTGTCTTAAAGTTGTTCTGCTGCTGGAATCTCTTATGTTATTAAGCTT 604
QY 1253 GCAAGAGATATCTTGTGACAGAGAAAGAGACG 1285
Db 605 GCAAGAGATATCTATGAGAAACAACCAAGAG 637

RESULT 15
AAC34062
ID AAC34062 standard; DNA; 829 BP.
XX AAC34062;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 5313.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX

OS Arabidopsis thaliana.
XX
XX EPI03405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 26-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
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Best Local Similarity 62.4%; Pred. No. 9.7e-37;
Matches 395; Conservative 0; Mismatches 236; Indels 2; Gaps 1;

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QY 713 AGGTCCCATCCCAACGCGCTGTCGCGAGCGCTGCGCGAGCTGACCTCACTCT 772
DB 65 AATCCCAATTCACACTTCTTACTGCTGGTGTGCTGAGTTAGCCAGACACTCT 124
QY 773 GCACCTATCCATGAGAGTCTGTCAGAACCCGCTTACCATGAGAAAGACGTGTACGA 832
DB 125 TGACATTAACCTCTTAATAGTACAGACTCGCTTACAAATTCAGAGAGTGTTCACAAAG 184
QY 833 ACCCTCCACAGCGTTGCTCAAGATCGTGGCGAGCAAGGCGCGGGAGCTGTACCGG 892
DB 135 GGAATTTGATGTCGTTTCTCAAAATCATACCGGAGAAAGACCCACAGAACTTACAGG 244
QY 893 GAGTCGCGCGAGCGCTGATCGCGTGTGTCGCTGACGCGCGGCGCACTTACGCGCTACG 952
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DB 305 ATTCTTTAGAAAGCATACCGAGATTCTTTTCAAAAGCAGAAAGATTGAAACATTGAGA 364
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Search completed: May 25, 2005, 06:55:31
Job time : 1318 secs

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 ACCESSION BT008958
 VERSION BT008958.1 GI:32128509
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 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 REFERENCE
 1 (bases 1 to 1625)
 Tingey,S.V., Wolters,P., Powell,M., Dolan,M., Miao,G.-H.,
 Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-2003) Crop Genetics, B. I. Dupont de Nemours and
 Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
 USA
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DEFINITION	Hordeum vulgare subsp. vulgare plastidial ADP-glucose transporter	
ACCESSION	mRNA, complete cds; nuclear gene for plastid product.	
VERSION	AJ560327	
KEYWORDS	AJ560327.1 GI:47156871	
SOURCE		
ORGANISM	'Hordeum vulgare' subsp. vulgare	
REFERENCE	Hordeum vulgare subsp. vulgare	
AUTHORS	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum. 1 (bases 1 to 1191) Patron,N.J., Greber,B., Fahy,B.F., Laurie,D.A., Parker,M.L. and Dwyer,K. The lys5 Mutations of Barley Reveal the Nature and Importance of Plastidial ADP-Glc Transporters for Starch Synthesis in Cereal Endosperm Plant Physiol. 135 (4), 2088-2097 (2004)	
JOURNAL	15299120	
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REFERENCE	Patron,N.J.	
TITLE	Direct Submission	
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 DB 274 GCGAAAGAGGCGCAAGAGCAGCTGAGTCTGAGGAGGTGAGGCTCAAGATCGGCAAC 333
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 LOCUS
 DEFINITION
 Oryza sativa (japonica cultivar-group) cDNA clone:002-127-B01, full insert sequence.
 ACCESSION
 AKI07368
 VERSION
 AKI07368.1 GI:3292577
 KEYWORDS
 FLI cDNA; oligo capping.
 SOURCE
 Oryza sativa (japonica cultivar-group)
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE
 1
 The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Oono, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Maeda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN: Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Komoto, H., Miyazaki, A., Oono, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
 Science 301 (5631), 376-379 (2003)
 JOURNAL
 MEDLINE
 PUBMED
 22752273
 12869764
 2 (bases 1 to 1662)
 REFERENCE
 ADACHI, J., AIZAWA, K., AKIMURA, T., ARAKAWA, T., CARNINCI, P., DOI, K., FUJIMURA, T., FUKUDA, S., HANAGAKI, T., HARA, A., HASHIDUME, W., HAYASHIDA, K., HAYASHIZAKI, Y., HAYATSU, N., HIRAMOTO, K., HIROAKA, T., HOTA, F., HOTTA, I., IIDA, J., IIDA, Y., IKEDA, R., IMAMURA, K., IMOTANI, K., ISHIBIKI, J., ISHII, Y., ISHIKAWA, M., ITOH, M., KAGAWA, I., KANAGAWA, S., KATOH, H., KAWAGASHIRA, N., KAWAI, J., KAWAMATA, M., KIKUCHI, S., KISHIKAWA-HIROZANE, T., KISHIMOTO, N., KOBAYASHI, M., KODAMA, T., KOJIMA, K., KOJIMA, Y., KONDO, S., KONNO, H., KONDA, M., KOYA, S., KURIBARA, C., KUROSAKI, T., KUSUMEGI, T., LI, C., LU, M., MAEDA, H., MATSUBARA, K., MATSUYAMA, T., MIURA, U., MIYAZAKI, A., MIZUNO, K., MURAKAMI, K., MURATA, M., NAGATA, T., NAKAMURA, M., NAMIKI, T., NARIKAWA, R., NIKURA, J., NISHI, K., NOMURA, K., NUMASAKI, R., OHNEDA, E., OHNO, M., OHTSUKI, K., OKA, M., OKA, H., OONO, N., OTA, Y., OONO, Y., RYU, R., SATOH, H., SAKAI, C., SAKAI, K., SAKAZUME, N., SANO, H., SASAKI, D., SATO, K., SATOH, K., SHIBATA, K., SHINAGAWA, A., SHIRAKI, T., SHISHIKI, T., SOGABE, Y., SUGANO, S., SUGIYAMA, A., SUZUKI, K., SUZUKI, Y., TAGAMI, M., TAGAMI-TAKEDA, Y., TAGAWA, A., TAKAHASHI, F., TAKAKU-KHACHI, S., TANAKA, T., TOMARU, A., TOYA, T., TSUNODA, Y., UEDA, M., WAKI, K., XIE, Q., YAHAGI, W., YAMADA, H., YAMAMOTO, M., YASUNISHI, A., YAZAKI, J., YOKOMIZO, S. and YOSHIMURA, A.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of

REFERENCE 2 (bases 1 to 927)
AUTHORS Villand, P. and Kleczkowski, L.A.
TITLE Direct Submission
JOURNAL Submitted (29-APR-2001) Dept. Plant Physiology, Umea University,
Umea 901 87, Sweden
FEATURES
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ACCESSION M79333.1
VERSION M79333.1 GI:168425
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1 (sites)
Nelson, O.E., Jr.
Dumas, B., Van Doorselaere, J., Legrand, M., Van Montagu, M. and
Inze, D.
TITLE Molecular analysis of a poplar O-methyltransferase involved in
lignin biosynthesis
JOURNAL Unpublished (1991)
REFERENCE 2 (bases 1 to 1733)
AUTHORS Sullivan, T.D., Strelow, L.I., Illingworth, C.A., Phillips, R.L. and
Nelson, O.E., Jr.
TITLE Analysis of maize brittle-1 alleles and a defective
Suppressor-mutator-induced mutable allele
JOURNAL Plant Cell 3 (12), 1337-1348 (1991)
MEDLINE 93005685
PUBMED 1668652
COMMENT Original source text: Zea mays (strain R802) Endosperm, 22 days
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ORIGIN

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Matches 810; Conservative 0; Mismatches 190; Indels 10; Gaps 2;
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LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:J033130A21, full
insert sequence.
ACCESSION
AK103471
VERSION
AK103471.1 GI:32988680
KEYWORDS
FLI CDNA; CAP trapper.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS
1 The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team:
Kikuchi, S., Satoh, K., Negata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Otsu, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurobaki, T., Kodama, T., Maeda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
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Saito, R., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,
Yoshino, M., and Hayashizaki, Y.
TITLE
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
JOURNAL
Science 301 (5631), 376-379 (2003)
MEDLINE
22752273
PUBMED
12869764
2 (bases 1 to 1968)
REFERENCE
AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
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Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
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Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nariikawa, R., Nikiura, J., Nihi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saesaki, D., Sato, K., Satoh, K., Shibata, K., Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., T., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

PLIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Iehibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariikawa, R., Nikiura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hamagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, D., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saesaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES
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Best Local Similarity 66.2%; Pred. No. 2.8e-51;
Matches 643; Conservative 0; Mismatches 325; Indels 3; Gaps 1;
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Db 827 CCATTTGAACGATTCAGACGCGCATTTGATGTGGGAGTAAATG--GAATTCGACCGG 883
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QY 676 AAGAAATACCTGACCCCGGAGCGCGGAGCCAGCCAAAGTCCCATCCCAAGCGCGTC 735
Db 1004 AACCAATTTTGAACCCCAATTCGAGGAGCAAAAGAAAGATCCCACTCCCTTACTA 1063
QY 736 GTGCGCGAGCGCTGCGCGGAGGCGTCAACCTTGACCTATCCATCGAGCTGTC 795
Db 1064 GTGGCTGGGAGCATTTCTGTGTGATGATTAACCTCTGATACCTCTGAAATTAAT 1123
QY 796 AAGACCCGTCCTACCATCGAAGAGAGCGTACGACAACTCTCCAGCGCTTGTCAAG 855
Db 1124 AAGACAGATTAACTATACATACAGAGAGGTATATGATTAATTTCTCACCGCTTGTCA 1183
QY 856 ATGTCGCGAGCAAGAGCCCGGAGGCTGTACCGCGGCTGGCGGAGCTGATCGCG 915
Db 1184 ATGTCCGTGAAGAAAGCCCTACTGAGCTGTACCGAGGTTTAAAGCAAGTTTAATTTGA 1243
QY 916 GTGTCGCGGATCGCGCGGCAACTTCTACGCTTACGAGACGCTGCGCGGCTGTACCG 975
Db 1244 GTTGTCCATATGCGCGGAGCAACTTCTGTCAGACACCTTAAAGAGCTTCAAG 1303
QY 976 CGGCGTCGCGGAAAGAGAGGTGGCAAGTCCGAGCTGTGATCGGTCGCGCGC 1035
Db 1304 AAGATTTCAAGAGCAATGAATAATCGGCAAGTTCCTACCTGCTCTTGGGTCGCGCGCA 1363
QY 1036 GGGGCTATGACGAGACGCGCACGTTCCCGCTGAGAGTGGCCGGAAGAGATGACAG 1095
Db 1364 GAGGCTATCTCAAGACACGCTCTTCCCTCGAGGTTGACGCAAGCATGCAAGTT 1423
QY 1096 GGGCGCGTGGGCGGAGGAGGTGTCAAGAAAGTGTCTGACGCGCATGTACTGATCTTC 1155
Db 1424 GCGCGAGTGTGTGCGAGGAGGTCTTCAAGAAATGATCTTCTCTGAGCATTTCTG 1483
QY 1156 GAGAAAGAGGAGCAACCGCGGCTCTACCGCGGCTGCGGCCAGCTGATCAAGTCAATG 1215
Db 1484 GAGGATGAAGGGGTGTGAGGGCTTTTACAGGGGCTTGGGCGCAAGTTGATGAAGTTGGTG 1543
QY 1216 CCGCGCGCGGCGATCTCTTCACTGTGTCTACGAGGCTTGAAGAAATCTTGTGACAG 1275
Db 1544 CCAGCGCGCGGTATTTGTTATGTGCTATGAGGCTTGAAGAAAGTATTTGACAGAGGA 1603
QY 1276 AAGAAAGACGG 1286
Db 1604 GAGGATGACTG 1614

RESULT 8
AR438062
LOCUS AR438062 1267 bp DNA linear PART 18-DEC-2003
DEFINITION Sequence 19 from patent US 6660850.
ACCESSION AR438062
VERSION AR438062.1 GI:40204513
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 1267)
AUTHORS Allen, S.M., Lightner, J.B. and Rafalski, J.A.
TITLE Nucleic acid encoding a wheat brittle-1 homolog
JOURNAL Patent: US 6660850-A 19 09-DEC-2003;
FEATURES
Location/Qualifiers
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/organism="unknown"

ORIGIN /mol_type="genomic DNA"

Query Match 24.6%; Score 400.2; DB 6; Length 1267;

Best Local Similarity 66.8%; Pred. No. 2.1e-46; Matches 586; Conservative 0; Mismatches 288; Indels 3; Gaps 1;

QY 415 AGGTCAGATCGGCAACCGGACCTGCGCGGCGCTGTCAGCGGCGCCATCGCGCGCGC 474
DB 2 AAGATTAGGTTGGGAATTCACACCTCAAGAGGCTCATAGTGGGGGATTGCAAGAGCA 61
QY 475 GTGTGAGAGCTTTGCTGCGCGCACTGAGACGATCAGACGCACTGATGTTGGGAGC 534
DB 62 GTGTCAAGAGACAGTTGTGGCGCTTTGAGACGATTAGACACATTTATGTCGGCAGC 121
QY 535 TCCGCGCGGACCTCCATGCGCGCGGCTTTCCGCTGATCATGCGACGAGGGGTGCGCC 594
DB 122 AATGGGAATTCATCTACGAGAGGTGTTGAC--TCCATCATGAMAGATGAGATGACT 178
QY 595 GGCCTCTTCCGGCGCAACCGCGTCACGTCCTCCGCTGCGCGCAAGGCAATCGAG 654
DB 179 GGGTGTTCGCGCGCAATTTGGTTATGTCATTCAGTGCCTCCGACGAAAGCAATCGAG 238
QY 655 CACTTCACCTTACGACACGCGGAGAGTACTGACCCCGAGGCGCGCGAGCCAGCCAG 714
DB 239 CTTTTCCTTTGATGATACGCTAAGAAAGTTCTTAACCCCAATCTGGGAGAGACAGAG 298
QY 715 GTCCCATCCCAACCGCGCTGTCGCGGAGCGCTGCGGAGTGGCTCAACCTGTGC 774
DB 299 ATCCCAATCCCTCTTCACTAGTGGGAGGCTTTTGTGCTGATGCTCACTCTGTGT 358
QY 775 ACCCTATCCATGAGAGTGTGTAAGACCGGCTCAACATGAGAGAGAGTGTACAGAC 834
DB 359 ACATACCTCTGGAATTAATAGACTGATTAACATACAGAGAGGTGTATGATTAAC 418
QY 835 CTCCTCAACGCTTCTGTAAGATCGTGCAGACGAGGCGCGGAGCTGTACCGCGG 894
DB 419 TTCCTCAATGATTTGTGAAATTTGTCGTGAAGAGGCTGTGAGCTGTATGAGGC 478
QY 895 CTGGCGCGGAGCTGATGCGCGCTGTGCTGCTGACGCGGCGCACTTCTACCGCTACG 954
DB 479 TTAAACCCCAAGTCTATCGAGTGTGTCATATGACGAAACCACTTCCGATATGAC 538
QY 955 AGCGTCGCGGAGTGTACCGCGCGCTGCGGAGAGAGAGAGTGTGGGAAACGTTCCGAG 1014
DB 539 ACCCTTAAGAGGTGTACAAAGAAATGTTCAGACCAATGAAATGCGCAACGTTCCAAC 598
QY 1015 CTGCTGATCGGCTCGCGCGGCGGCGCATAGCCAGACGCGCAACGTTCCGCTGAGTG 1074
DB 599 CTGCTCATTTGGGTCTGTGACGAGAGCCATCTCAAGCATCTTCTCTCAAGGTT 658
QY 1075 GCGCGGAGACAGATGAGGTGGGCGCGCTGTGGCGGAGGAGGTGTACAGAACGTCGT 1134
DB 659 GCTCGCAACCATGTGAGTGTGAGTGTGGCGCGCGGAGGTATACAGAAACATGCTT 718
QY 1135 CACGCTATGTATCTGATCTCTCGAAGAGAGGCAACCGCGGCTCTACCGCGGCTCGGC 1194
DB 719 CACGCTCTCTGACCAATCTCGAGAGCAGAAAGGGGCTTCTACAGAGAGACTGGG 778
QY 1195 CCGAGCTGATCAAGCTCAATGCGCGCGCGGCGCATCTCTTATGATGATCAAGGCGTTC 1254
DB 779 CCTAGTGTGATAGAGTGTGCTGCTGTGCTGTGGGATTTCTTTATGTGTCTACAGAGCTTC 838
QY 1255 AAGAAAGATCTTGTGACGAGAAAGAGAGCGCGCG 1291
DB 839 AAGAGATCTGATTTGAGAGAGAGAGAGATGAGCG 875

RESULT 9
LOCUS BT009587 1267 bp mRNA linear PLN 20-JUN-2003
DEFINITION Trifolium aestivum clone wrein.pk0049.el:fls, full insert mRNA
sequence.

ACCESSION BT009587
VERSION BT009587.1 GI:32129138

KEYWORDS

FLI CDNA.

SOURCE

Trifolium aestivum (bread wheat)

ORGANISM

Trifolium aestivum

REFERENCE

1 (bases 1 to 1267)

AUTHORS

Tingey, S.V., Woltere, P., Powell, M., Dolan, M., Mao, G.-H.,

Careher, N.R., Hanafey, M.K. and Haney, C.F.

Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and

Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,

USA

FEATURES

Location/Qualifiers

source

1..1267

/organism="Trifolium aestivum"

/mol_type="mRNA"

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/clone="wrein.pk0049.el:fls"

ORIGIN

Query Match 24.6%; Score 400.2; DB 8; Length 1267;

Best Local Similarity 66.8%; Pred. No. 2.1e-46; Matches 586; Conservative 0; Mismatches 288; Indels 3; Gaps 1;

QY 415 AGGTCAGATCGGCAACCGGACCTGCGCGGCGCTGTCAGCGGCGCCATCGCGCGCGC 474
DB 2 AAGATTAGGTTGGGAATTCACACCTCAAGAGGCTCATAGTGGGGGATTGCAAGAGCA 61
QY 475 GTGTGAGAGACTTTGCTGCGCGCACTGAGACGATCAGACGCACTGATGTTGGGAGC 534
DB 62 GTGTCAAGAGACAGTTGTGGCGCTTTGAGACGATTAGACACATTTGATGTCGGCAGC 121
QY 535 TCCGCGCGGACCTCCATGCGCGCGGCTTTCCGCTGATCATGCGACGAGGGGTGCGCC 594
DB 122 AATGGGAATTCATCTACGAGAGGTGTTGAC--TCCATCATGAMAGATGAGATGACT 178
QY 595 GGCCTCTTCCGGCGCAACCGCGTCAAGCTCTCGCGTGTGCGCGCAAGGCAATCGAG 654
DB 179 GGGTGTTCGCGCGCAATTTGGTTATGTCATTCAGTGCCTCCGACGAAAGCAATCGAG 238
QY 655 CACTTCACCTTACGACACGCGGAGAGTACTGACCCCGAGGCGCGGAGCCAGCCAG 714
DB 239 CTTTTCCTTTGATGATACGCTAAGAAAGTTCTTAACCCCAATCTGGGAGAGACAGAG 298
QY 715 GTCCCATCCCAACCGCGCTGTCGCGGAGCGCTGCGGAGTGGCTCAACCTGTGC 774
DB 299 ATCCCAATCCCTCTTCACTAGTGTGACGAGAGCTTTTGTGCTGATCACTCAAGTGTGT 358
QY 775 ACCCTATCCATGAGAGTGTGTAAGACCGGCTCAACATGAGAGAGAGTGTACAGAC 834
DB 359 ACATACCTCTGGAATTAATAGACTGATTAACATACAGAGAGGTGTATGATTAAC 418
QY 835 CTCCTCAACGCTTCTGTAAGATCGTGCAGACGAGGCGCGGAGCTGTACCGCGG 894
DB 419 TTCCTCAATGATTTGTGAAATTTGTCGTGAAGAGGCTTCTGACCTGTATGAGGC 478
QY 895 CTGGCGGAGCTGATGCGCGCTGTGCTGCTGACGCGGCGCACTTCTACCGCTACGAG 954
DB 479 TTAAACCCCAAGTCTATGAGTGTGACGAGAGCCATCTCAAGCATCTTCTCTCAAGGTT 538
QY 955 AGCGTCGCGGAGTGTACCGCGCGCTGTGGGAGAGAGAGTGTGGGAAACGTTCCGAG 1014
DB 539 ACCCTTAAGAGGTGTACAAAGAAATGTTCAGAGCAATGAAATGCGCAACGTTCCAAC 598
QY 1015 CTGCTGATCGGCTCGCGCGGCGGCGCATAGCCAGACGCGCAACGTTCCGCTGAGTG 1074
DB 599 CTGCTCATTTGGGTCTGTGACGAGAGCCATCTCAAGCATCTTCTCTCAAGGTT 658
QY 1075 GCGCGGAGACAGATGAGGTGGGCGCGCTGTGGCGGAGGAGGTGTACAGAACGTCGT 1134

Db	659	GCTGCGAAGCAACATGCAAGTCGAGAGCTGTTGGCCGCGAGAAAGTATACAAAGCAATGCTT	718
Qy	1135	CACGCCATGTACTGCATCTCTGGAGAGAGGACCCGCCGAGCTTACCGCGGGCTCGGC	1194
Db	719	CACGCTCTCCCGAACCATTCCTCGAGAGCAAGAGGGGTTGGGGGCGCTCTACAGAGACTGGGG	778
Qy	1195	CCCAAGCTGCATCAAGCTCATGCGCCGCGCGCATCTGCTTCATGTGCTACAGAGGCTGCG	1254
Db	779	CTTAGTTGCATGAAAGCTGTGTGCTGCTCTGCGAATTTGTTTATGTGCTTACGAAGCTTGC	838
Qy	1255	AAGAAGATACTTGTGCGACGAGAAAGAAAGACGGCGCG	1291
Db	839	AAGAAGATACTGATGTAGAGAAAGAAAGAAATGAACG	875
RESULT 10			
LOCUS	AR438060	449 bp	DNA
DEFINITION	Sequence 15 from patent US 6660850.		linear
ACCESSION	AR438060		
VERSION	AR438060.1	GI:40204511	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 449)		
TITLE	Allen, S.M., Lightner, J.E. and Rafalecki, J.A.		
JOURNAL	Nucleic acid encoding a wheat brittle-1 homolog		
FEATURES	Patent: US 6660850-A 15 09-DEC-2003;		
SOURCE	Location/Qualifiers		
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	/organism="unknown"		
	/mol_type="genomic DNA"		
ORIGIN			
Query Match 24.2%; Score 392.6; DB 6; Length 449;			
Best Local Similarity 96.4%; Pred. No. 2.7e-45;			
Matches 432; Conservative 0; Mismatches 12; Indels 4; Gaps 3;			
Qy	1	GGCCAGTGGAGGAGTGAAGACTGTAAGAACTCTTAGAGGAGCAAGTATCAGTTCTGTCT	60
Db	1	GGCCANTGAGGGAGTGAAGAGACTGAAGAACTCTTAGGACGGGCAAGTATCAGTTCTGTCT	60
Qy	61	TGCTTCTCTCG-AGATGGCGGGCGGCATATGCGCGAGCAATGTTGACCAAGAACACCG	119
Db	61	TGCTTCTCTCGAAGATGGCGGGCGGCATATGCGCGAGCAATGTTGACCAAGAACACCG	120
Qy	120	CGCCTCGCTCGTCATGAGCAAGAAAGACTGTTATTGGGGCCGGTCCCTGAGGTGCGCTT	179
Db	121	CGCCTCGCTCGTCATGAGCAAGAAAGACTGTTATTGGGGCCGGTCCCTGAGGTGCGCTT	180
Qy	180	CCCTTGGAGCTGCGAGCCCGAGTCCAGAGACTTGGACTTCCACGACGAGGCTGTGTTGCG	239
Db	181	CCCTTGGAGCTGCGAGCCCGAGTCCAGAGACTTGGACTTCCACGACGAGGCTGTGTTGCG	240
Qy	240	CAGCGTGGACTCAGCTCTGTCCACAGCGGCGCCGCGGTAGCGCGCGAGCATAGACGGAA	299
Db	241	CAGCGTGGAGACTCAGCTCTGTCCACAGCGGCGCCGCGGTAGCGCGCGAGCATAGACGGAA	300
Qy	300	GGCTGGGGCCCGGACGACGTGCGACAC-AGCTGCGAGCGCGGGGCGAGGGCGGGCGTCC	358
Db	301	GGCTGGGGCCCGGACGACGTGTCACACCAAGCTGCAATCGCGGGGCGAGGGGGCGTCC	360
Qy	359	AGAAAGCCACGAAAGCGCAAAAAAGCGCAAAAAAGCAGACTGAGTGTGA--GGAGGTGAG	416
Db	351	AGAAAGCCCAAGAGCGCAAAAAAGCGCAAAAAAGCAGACTGAGTGTGAAGAGAGGTGAG	420
Qy	417	GGTCAAGATCGGCAACCCGCACTTGGC	444
Db	421	GGTCAAGATCGGCAACCCGCACTTGGC	448
RESULT 11			

LOCUS	LOCUS	102230 bp	DNA	linear	PLN 15-APR-2004
AP004045	Oryza sativa (japonica cultivar-group)			genomic DNA,	chromosome 2,
DEFINITION	Oryza sativa (japonica cultivar-group)			genomic DNA,	chromosome 2,
AP004045	BAC clone:OU1135_F06.				
ACCESSION	AP004045				
VERSION	AP004045.3	GI:46390078			
KEYWORDS					
SOURCE					
ORGANISM	Oryza sativa (japonica cultivar-group)				
REFERENCE	Oryza sativa (japonica cultivar-group)				
1	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.				
AUTHORS	Sasaki, T., Matsumoto, T. and Yamamoto, K.				
TITLE	Oryza sativa n1pnpbare(GA3) genomic DNA, chromosome 2, BAC clone:OU1135_F06				
JOURNAL	Published Only in Database (2001)				
AUTHORS	2 (bases 1 to 102230)				
TITLE	Sasaki, T., Matsumoto, T. and Yamamoto, K.				
JOURNAL	Direct Submission				
COMMENT	Submitted (15-AUG-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kamondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rpg.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468) On Apr 14, 2004 this sequence version replaced g1:38347815. Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mlt.edu/GENSCAN.html), PSENESH (http://www.softberry.com/), Genemark_hmm (http://opal.biology.gatech.edu/Genemark/), glimmerM (http://www.tigr.org/cdb/glimmerx/glmr form.html), RiceHMM (http://rpg.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4 (http://globin.cse.psu.edu/html/docs/sim4.html), gap2 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cdna sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI Nonredundant Protein database with BLASTP. ESTs represent the identified cdna sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cdna sequences using BLASTN with the corresponding DDBJ accession no.				
	A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cdna or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.				
	The orientation of the sequence is from -21M3 to M3rev of the BAC clone. This sequence of OU1135_F06 clone has an overlap with P0419A09 (DDBJ: AP004869) clone at 5' end and with P054HH11 (DDBJ: AP005008) clone at 3' end. The sequence was generated by combining Monsanto and RGP-Japan sequencing data. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rpg.dna.affrc.go.jp/Genomeseq.html.				
FEATURES	Location/Qualifiers				
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	/chromosome="2"				
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	/gene="OU1135_F06.1"				
misc_feature	complement(11735..21686)				
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probably inactive due to no termination codon in CDS"
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/note="start and end point are not identified"
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this category is not included in IRGSP standard"
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KLP1PVLVAGALAGVASTLCTYPMELVTRLTLEKDVNDLHAFVKIVRGGSEL
VRLGAPSLIGVPAATNFYAYETLRILVLRATGRADVPAAITLLIGSAAAGSTAL
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similar to Oryza sativa chromosome 1, OSUBA0089K24.4"
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/note="hypothetical ORF

predicted by GeneMark.hmm
this category is not included in IRGSP standard"
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/note="supported by full-length cDNA (s) : AK068376"
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37446..37628))
/gene="OJ1135_F06.7"
/note="supported by full-length cDNA (s) : AK099277"
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37446..37544))
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AK101844, AK068376, AK099277
similar to Arabidopsis thaliana chromosome 2, AC2925570"
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VAEVPADVHHPAAAGSVLLDHATGVVIGFAVVGDDVSIHHVTLLGOTGEAVDRH
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Query Match 22.3%; Score 362.8; DB 8; Length 102230;
Best Local Similarity 85.7%; Pred. No. 1.9e-41;
Matches 403; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 810 CATGAGAAAGACGTGTACGACACCTCTCCAGCCGTTTCGCAAGATCTGCGGAGCA 869
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QY 870 AGGCGGGGAGCGTACCGGGGCTGACGCGCGGAGCTGATCGGCGTGTGTCGCGTACGC 929
DB 27553 CGGCGGGGAGCGTACCGGGGCTGACGCGCGGAGCTGATCGGCGTGTGTCGCGTACGC 27612
QY 930 GCGCGCAACTTCTTACGCGCTACGAGACGCTGCGCGCGCTGTACCGCGCGCGCTCGGGGAA 989
DB 27613 GCGCGCAACTTCTTACGCGCTACGAGACGCTGCGCGCGCTGTACCGCGCGCGCGCGG 27672
QY 990 AGAGAGGTGGCAACGTCCGACGCTGTATCGGCTCCGCGGGGCGGCGCATAGCCAG 1049

Accession	Sequence	Position
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Qy	1050 CACGGCCACGTTCCCGCTGAGAGTGGCGCGGACAGATCAGGTGGCGCGTCGGCCG	1109
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ACCESSION	AP004873				
VERSION	AP004873.2	GI:21280398			
KEYWORDS	HTG; HTGS; PHASE2.				
SOURCE	<i>Oryza sativa</i> (japonica cultivar-group)				
ORGANISM	<i>Oryza sativa</i> (japonica cultivar-group)				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.				

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS JOURNAL	
1 Sasaki, T., Matsumoto, T. and Yamamoto, K. <i>Oryza sativa</i> nipponbare (GA3) genomic DNA, chromosome 2, PAC clone, P0453609 Published Only in Database (2002) 2 (bases 1 to 136289) Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission Submitted (20-MAR-2002) Takuji Sasaki, National Institute of	

JOURNAL Submitted (20-MAR-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kamondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp), URL:<http://vsgp.dna.affrc.go.jp/>,
Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT On May 30, 2002 this sequence version replaced gi:19698293.
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

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RESULT 13
AP004869
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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AUTHORS
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JOURNAL
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AUTHORS
TITLE
COMMENT

AP004869 168064 bp DNA linear PLN 15-APR-2004
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2, PAC clone: P0419A09.
AP004869
AP004869.3 GI:46390373
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyte; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Oryza sativa nipponbare (Ga3) genomic DNA, chromosome 2, PAC clone: P0419A09
2 Published Only in Database (2002)
2 (bases 1 to 168064)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Direct Submission
Submitted (20-MAR-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://xgp.dna.affrc.go.jp/, Tel: 81-226-38-7441, Fax: 81-226-38-7468)
On Apr 14, 2004 this sequence version replaced gi:39725615.

JOURNAL
Submitted (20-MAR-2002) Takuya Sasaki, National Institute of
Parasitological Sciences, Rice Genome Research Program, Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
[E-mail:tsasaka@nias.affrc.go.jp, URL:<http://rpg.dna.affrc.go.jp/>,
Tel:81-298-38-7441, Fax:81-298-38-7468]
On Apr 14, 2004 this sequence version replaced gi:339725615.
Genes were predicted from the integrated results of the following:
GENSCAN (<http://CCR-081.mit.edu/GENSCAN.html>), FGENESH
(<http://www.softberry.com/>), GeneMark.hmm
(<http://opal.biology.gatech.edu/GeneMark/>), Glimmer
(http://www.cgl.rg.cdb.gliimern/glimr_form.html), RiceHMM
(<http://rpg.dna.affrc.go.jp/RiceHMM/>), SplicePredictor
(<http://bioinformatics.laestate.edu/cgi-bin/sp.cgi>), siima
(<http://globin.cse.psu.edu/html/docs/siima.html>), gap2
(<http://www.tigr.org/software/glimmer/>), BLASTX and BLASTY. The
genomic sequence was searched against NCBI Nonredundant Protein
database, nr (<ftp://ncbi.nlm.nih.gov/blast/db>) and the cDNA
sequence database at RGP or DDBJ. Protein homologs of the coding
regions were searched against NCBI Nonredundant Protein database
with BLASTP. ESTs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no. and RGP clone ID

Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant accession to a protein is classified based on the protein name to indicate the homology level such as name name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to RGSF standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0419A09 clone has an overlap with P0026H03 (DDBJ: AP004812) clone at 5' end and with OJ113_F06 (DDBJ: AP004865) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rsgp.dna.affrc.go.jp/genomeseq.html>.

FEATURES

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REFERENCE	1 (bases 1 to 1179)					
AUTHORS	Chen, R., Chen, H., Kim, C.-J., Meyers, M. C., Ban, J., Bowser, L.,					
	Carinci, P., Chang, E., Dale, J. M., Goldsmith, A. D., Hayashizaki, Y.,					
	Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,					
	Lam, B., Lee, J. M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,					
	Onodera, C. S., Palm, C. J., Quach, H. L., Sakurai, T., Saito, M., Seki, M.,					
	Southwick, A., Tang, C. C., Tortolani, M., Wu, H. C., Yamada, K.,					
	Yamamura, Y., Yu, G., Yu, S., Shimozaki, K., Davis, R. W., Theologis, A.					
	and Ecker, J. R.					

TITLE
JOURNAL
REFERENCE
AUTHORS

Arabidopsis cDNA clones
Unpublished
2 (bases 1 to 1179)
Cheuk,R., Chen,H., Kim,C.J., Meyers,M.C., Banh,J., Bowser,l.,
Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jones,T., Kamiya,A., Karlín-Neumann,G., Kawai,J.,
Iam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M.,
Onodera,C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C.,
Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K.,
Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A.,
and Ecker,J.R.
Direct Submission
Submitted (14-JUN-2002) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFI cDNAs (RAFI cDNA : 'RIKEN
Arabidopsis Full-Length cDNA.') : Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

COMMENT

The Salk, Stanford, PGSC (SSP) Consortium members carried out the
sequencing and annotation of the RAFI cDNAs: Cheuk,R., Chen,H.,
Kim,C.J., Meyers,M.C., Shih,P., Banh,J., Bowser,l., Dale,J.M.,
Goldsmith,A.D., Jiang,P.X., Jones,T., Karlín-Neumann,G., Lam,B.,
Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S.,
Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C.,
Toriumi,M., Yamada,K., Yamamura, Y., Yu,G., Yu,S., Davis,R.W.,
Theologis,A., and Ecker,J.R.

FEATURES

source

Chouk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.
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ORIGIN

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 VERSION
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 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 1334)
 Haase, B.J., Volkovskiy, N., Town, C.D., Troukhan, M., Alexandrov, N.,
 Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
 Full-length messenger RNA sequences greatly improve genome
 annotation
 JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)

MEDLINE 22088475
 PUBMED 12093376
 REFERENCE 2 (bases 1 to 1334)
 AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
 TITLE Full-length cDNA from Arabidopsis thaliana
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1334)
 AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
 COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Geneset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
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ORIGIN
 Query Match 22.0%; Score 357.8; DB 8; Length 1334;
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